<110> Lindquist, Susan
       Li, Liming
       Ma, Jiyan
       Liu, Jia-Jia
       Sondheimer, Neal
       Scheibel, Thomas

<120> RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS
       AND METHODS COMPRISING SAME

<130> 30554/34978A

<140> 09/591,632
<141> 2000-06-09

<150> US 06/138,833
<151> 1999-06-09

<160> 65

<170> PatentIn Ver. 2.0

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attggagttt gaagaaaatc ccaaccctac ggtagaaaat tgaatatcgt atctgtttat 180

acacacatac atacatttat atttataata agcgttaaaa tttcggcaga atatctgtca 240

accacacaaa aatcatacaa cgaatggtat atgcttcatt tctttgtttc gcattagctg 300

cgctatttga ctcaaattat tattttttac taagacgacg cgtcacagtg ttcgagtctg 360

tgtcatttct tttgtaattc tcttaaacca cttcataaag ttgtgaagtt catagcaaaa 420

ttcttccgca aaaagatgaa tcttagttct cagcccacca aagaggtac atgctaagat 480

catacagaag ttattgtcac ttcttacctt gctcttaaat gtacattaca accgggtatt 540

atatcttaca tcatcgtata atatgatctt tctttatgga gaaaatтttt ttttcactcg 600

accaaagctc ccattgcttc tgaagagtgt agtgtatatt ggtacatctt ctcttgaaag 660

actccattgt actgtaacaa aaagcggttt cttcatcgac ttgctcggaa taacatctat 720

atctgcccac tagcaaca atg tcg gat tca aac caa ggc aac aat cag caa   771
                        Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln
                         1   5   10

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aac tac cag caa tac agc cag aac ggt aac caa caa caa ggt aac aac    819
Asn Tyr Gln Gln Tyr Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn
              15                  20                  25

aga tac caa ggt tat caa gct tac aat gct caa gcc caa cct gca ggt    867
Arg Tyr Gln Gly Tyr Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly
              30                  35                  40

ggg tac tac caa aat tac caa ggt tat tct ggg tac caa caa ggt ggc    915
Gly Tyr Tyr Gln Asn Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly
          45                  50                  55

tat caa cag tac aat ccc gac gcc ggt tac cag caa cag tat aat cct    963
Tyr Gln Gln Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro
60                  65                  70                  75

caa gga ggc tat caa cag tac aat cct caa ggc ggt tat cag cag caa   1011
Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln
              80                  85                  90

ttc aat cca caa ggt ggc cgt gga aat tac aaa aac ttc aac tac aat   1059
Phe Asn Pro Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn
              95                 100                 105

aac aat ttg caa gga tat caa gct ggt ttc caa cca cag tct caa ggt   1107
Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly
          110                 115                 120

atg tct ttg aac gac ttt caa aag caa caa aag cag gcc gct ccc aaa   1155
Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys
          125                 130                 135

cca aag aag act ttg aag ctt gtc tcc agt tcc ggt atc aag ttg gcc   1203
Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala
140                 145                 150                 155

aat gct acc aag aag gtt ggc aca aaa cct gcc gaa tct gat aag aaa   1251
Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys
              160                 165                 170

gag gaa gag aag tct gct gaa acc aaa gaa cca act aaa gag cca aca   1299
Glu Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr
              175                 180                 185

aag gtc gaa gaa cca gtt aaa aag gag gag aaa cca gtc cag act gaa   1347
Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu
              190                 195                 200

gaa aag acg gag gaa aaa tcg gaa ctt cca aag gta gaa gac ctt aaa   1395
Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys
          205                 210                 215

atc tct gaa tca aca cat aat acc aac aat gcc aat gtt acc agt gct   1443
Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala
220                 225                 230                 235

gat gcc ttg atc aag gaa cag gaa gaa gaa gtg gat gac gaa gtt gtt   1491
Asp Ala Leu Ile Lys Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val
              240                 245                 250

aac gat atg ttt ggt ggt aaa gat cac gtt tct tta att ttc atg ggt   1539
Asn Asp Met Phe Gly Gly Lys Asp His Val Ser Leu Ile Phe Met Gly
          255                 260                 265
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- 2 -

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cat gtt gat gcc ggt aaa tct act atg ggt ggt aat cta cta tac ttg     1587
His Val Asp Ala Gly Lys Ser Thr Met Gly Gly Asn Leu Leu Tyr Leu
        270             275             280

act ggc tct gtg gat aag aga act att gag aaa tat gaa aga gaa gcc     1635
Thr Gly Ser Val Asp Lys Arg Thr Ile Glu Lys Tyr Glu Arg Glu Ala
        285             290             295

aag gat gca ggc aga caa ggt tgg tac ttg tca tgg gtc atg gat acc     1683
Lys Asp Ala Gly Arg Gln Gly Trp Tyr Leu Ser Trp Val Met Asp Thr
300             305             310             315

aac aaa gaa gaa aga aat gat ggt aag act atc gaa gtt ggt aag gcc     1731
Asn Lys Glu Glu Arg Asn Asp Gly Lys Thr Ile Glu Val Gly Lys Ala
                320             325             330

tac ttt gaa act gaa aaa agg cgt tat acc ata ttg gat gct cct ggt     1779
Tyr Phe Glu Thr Glu Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly
                335             340             345

cat aaa atg tac gtt tcc gag atg atc ggt ggt gct tct caa gct gat     1827
His Lys Met Tyr Val Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp
        350             355             360

gtt ggt gtt ttg gtc att tcc gcc aga aag ggt gag tac gaa acc ggt     1875
Val Gly Val Leu Val Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly
        365             370             375

ttt gag aga ggt ggt caa act cgt gaa cac gcc cta ttg gcc aag acc     1923
Phe Glu Arg Gly Gly Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr
380             385             390             395

caa ggt gtt aat aag atg gtt gtc gtc gta aat aag atg gat gac cca     1971
Gln Gly Val Asn Lys Met Val Val Val Val Asn Lys Met Asp Asp Pro
                400             405             410

acc gtt aac tgg tct aag gaa cgt tac gac caa tgt gtg agt aat gtc     2019
Thr Val Asn Trp Ser Lys Glu Arg Tyr Asp Gln Cys Val Ser Asn Val
                415             420             425

agc aat ttc ttg aga gca att ggt tac aac att aag aca gac gtt gta     2067
Ser Asn Phe Leu Arg Ala Ile Gly Tyr Asn Ile Lys Thr Asp Val Val
            430             435             440

ttt atg cca gta tcc ggc tac agt ggt gca aat ttg aaa gat cac gta     2115
Phe Met Pro Val Ser Gly Tyr Ser Gly Ala Asn Leu Lys Asp His Val
        445             450             455

gat cca aaa gaa tgc cca tgg tac acc ggc cca act ctg tta gaa tat     2163
Asp Pro Lys Glu Cys Pro Trp Tyr Thr Gly Pro Thr Leu Leu Glu Tyr
460             465             470             475

ctg gat aca atg aac cac gtc gac cgt cac atc aat gct cca ttc atg     2211
Leu Asp Thr Met Asn His Val Asp Arg His Ile Asn Ala Pro Phe Met
                480             485             490

ttg cct att gcc gct aag atg aag gat cta ggt acc atc gtt gaa ggt     2259
Leu Pro Ile Ala Ala Lys Met Lys Asp Leu Gly Thr Ile Val Glu Gly
            495             500             505

aaa att gaa tcc ggt cat atc aaa aag ggt caa tcc acc cta ctg atg     2307
Lys Ile Glu Ser Gly His Ile Lys Lys Gly Gln Ser Thr Leu Leu Met
            510             515             520
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cct aac aaa acc gct gtg gaa att caa aat att tac aac gaa act gaa      2355
Pro Asn Lys Thr Ala Val Glu Ile Gln Asn Ile Tyr Asn Glu Thr Glu
    525                 530                 535

aat gaa gtt gat atg gct atg tgt ggt gag caa gtt aaa cta aga atc      2403
Asn Glu Val Asp Met Ala Met Cys Gly Glu Gln Val Lys Leu Arg Ile
540                 545                 550                 555

aaa ggt gtt gaa gaa gaa gac att tca cca ggt ttt gta cta aca tcg      2451
Lys Gly Val Glu Glu Glu Asp Ile Ser Pro Gly Phe Val Leu Thr Ser
                560                 565                 570

cca aag aac cct atc aag agt gtt acc aag ttt gta gct caa att gct      2499
Pro Lys Asn Pro Ile Lys Ser Val Thr Lys Phe Val Ala Gln Ile Ala
            575                 580                 585

att gta gaa tta aaa tct atc ata gca gcc ggt ttt tca tgt gtt atg      2547
Ile Val Glu Leu Lys Ser Ile Ile Ala Ala Gly Phe Ser Cys Val Met
            590                 595                 600

cat gtt cat aca gca att gaa gag gta cat att gtt aag tta ttg cac      2595
His Val His Thr Ala Ile Glu Glu Val His Ile Val Lys Leu Leu His
    605                 610                 615

aaa tta gaa aag ggt acc aac cgt aag tca aag aaa cca cct gct ttt      2643
Lys Leu Glu Lys Gly Thr Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe
620                 625                 630                 635

gct aag aag ggt atg aag gtc atc gct gtt tta gaa act gaa gct cca      2691
Ala Lys Lys Gly Met Lys Val Ile Ala Val Leu Glu Thr Glu Ala Pro
                640                 645                 650

gtt tgt gtg gaa act tac caa gat tac cct caa tta ggt aga ttc act      2739
Val Cys Val Glu Thr Tyr Gln Asp Tyr Pro Gln Leu Gly Arg Phe Thr
            655                 660                 665

ttg aga gat caa ggt acc aca ata gca att ggt aaa att gtt aaa att      2787
Leu Arg Asp Gln Gly Thr Thr Ile Ala Ile Gly Lys Ile Val Lys Ile
            670                 675                 680

gcc gag taa atttcttgca aacataagta aatgcaaaca caataatacc             2836
Ala Glu
    685

gatcataaag cattttcttc tatattaaaa aacaaggttt aataaagctg ttatatatat 2896

atatatatat atagacgtat aattagttta gttctttttg taccatatac cataaacaag 2956

gtaaacttca cctctcaata tatctagaat ttcataaaaa tatctagcaa ggtttcaact 3016

ccttcaatca cgttttcatc ataacccttc cccggcgtta tttcagaatg tgcaaaatct 3076

attagtgaca tggaactcaa agaaccagtt gttttttttgt cctttggtcc ttcgctgctt 3136

ccctcggcat catcatcatc atcatcatca ttatcatcat cgtcgtcatc atcgtctata 3196

aaatcatctc gcataagttt gtcaacatca tttagtaatt cccatcgctc cgggtctcct 3256

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taaaa                                                              3321
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             20                  25                  30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
         35                  40                  45

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
     50                  55                  60

Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln
 65                  70                  75                  80

Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro Gln Gly
             85                  90                  95

Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly
            100                 105                 110

Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu Asn Asp
        115                 120                 125

Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu
    130                 135                 140

Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys
145                 150                 155                 160

Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser
            165                 170                 175

Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu Glu Pro
            180                 185                 190

Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr Glu Glu
            195                 200                 205

Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu Ser Thr
    210                 215                 220

His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu Ile Lys
225                 230                 235                 240

Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp Met Phe Gly
            245                 250                 255

Gly Lys Asp His Val Ser Leu Ile Phe Met Gly His Val Asp Ala Gly
            260                 265                 270

Lys Ser Thr Met Gly Gly Asn Leu Leu Tyr Leu Thr Gly Ser Val Asp
        275                 280                 285

Lys Arg Thr Ile Glu Lys Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg
    290                 295                 300
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-5-

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Gln Gly Trp Tyr Leu Ser Trp Val Met Asp Thr Asn Lys Glu Glu Arg
305                 310             315                     320

Asn Asp Gly Lys Thr Ile Glu Val Gly Lys Ala Tyr Phe Glu Thr Glu
                325             330                 335

Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly His Lys Met Tyr Val
            340             345                 350

Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp Val Gly Val Leu Val
        355             360                 365

Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly Phe Glu Arg Gly Gly
    370             375                 380

Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr Gln Gly Val Asn Lys
385                 390             395                     400

Met Val Val Val Val Asn Lys Met Asp Asp Pro Thr Val Asn Trp Ser
            405             410                 415

Lys Glu Arg Tyr Asp Gln Cys Val Ser Asn Val Ser Asn Phe Leu Arg
            420             425                 430

Ala Ile Gly Tyr Asn Ile Lys Thr Asp Val Val Phe Met Pro Val Ser
        435             440                 445

Gly Tyr Ser Gly Ala Asn Leu Lys Asp His Val Asp Pro Lys Glu Cys
    450             455                 460

Pro Trp Tyr Thr Gly Pro Thr Leu Leu Glu Tyr Leu Asp Thr Met Asn
465             470             475                     480

His Val Asp Arg His Ile Asn Ala Pro Phe Met Leu Pro Ile Ala Ala
            485             490                 495

Lys Met Lys Asp Leu Gly Thr Ile Val Glu Gly Lys Ile Glu Ser Gly
        500             505                 510

His Ile Lys Lys Gly Gln Ser Thr Leu Leu Met Pro Asn Lys Thr Ala
    515             520                 525

Val Glu Ile Gln Asn Ile Tyr Asn Glu Thr Glu Asn Glu Val Asp Met
    530             535                 540

Ala Met Cys Gly Glu Gln Val Lys Leu Arg Ile Lys Gly Val Glu Glu
545             550             555                     560

Glu Asp Ile Ser Pro Gly Phe Val Leu Thr Ser Pro Lys Asn Pro Ile
            565             570                 575

Lys Ser Val Thr Lys Phe Val Ala Gln Ile Ala Ile Val Glu Leu Lys
        580             585                 590

Ser Ile Ile Ala Ala Gly Phe Ser Cys Val Met His Val His Thr Ala
    595             600                 605

Ile Glu Glu Val His Ile Val Lys Leu Leu His Lys Leu Glu Lys Gly
    610             615                 620

Thr Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe Ala Lys Lys Gly Met
625             630             635                     640
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Lys Val Ile Ala Val Leu Glu Thr Glu Ala Pro Val Cys Val Glu Thr
                645                 650                 655

Tyr Gln Asp Tyr Pro Gln Leu Gly Arg Phe Thr Leu Arg Asp Gln Gly
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Thr Thr Ile Ala Ile Gly Lys Ile Val Lys Ile Ala Glu
            675                 680                 685


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agtttttcat tttttgttat tagtcatatt gttttaagct gcaaattaag ttgtacacca 180

a atg atg aat aac aac ggc aac caa gtg tcg aat ctc tcc aat gcg ctc 229
  Met Met Asn Asn Asn Gly Asn Gln Val Ser Asn Leu Ser Asn Ala Leu
    1               5                  10                  15

cgt caa gta aac ata gga aac agg aac agt aat aca acc acc gat caa   277
Arg Gln Val Asn Ile Gly Asn Arg Asn Ser Asn Thr Thr Thr Asp Gln
                20                  25                  30

agt aat ata aat ttt gaa ttt tca aca ggt gta aat aat aat aat aat   325
Ser Asn Ile Asn Phe Glu Phe Ser Thr Gly Val Asn Asn Asn Asn Asn
            35                  40                  45

aac aat agc agt agt aat aac aat aat gtt caa aac aat aac agc ggc   373
Asn Asn Ser Ser Ser Asn Asn Asn Asn Val Gln Asn Asn Asn Ser Gly
        50                  55                  60

cgc aat ggt agc caa aat aat gat aac gag aat aat atc aag aat acc   421
Arg Asn Gly Ser Gln Asn Asn Asp Asn Glu Asn Asn Ile Lys Asn Thr
65                  70                  75                  80

tta gaa caa cat cga caa caa caa cag gca ttt tcg gat atg agt cac   469
Leu Glu Gln His Arg Gln Gln Gln Gln Ala Phe Ser Asp Met Ser His
                85                  90                  95

gtg gag tat tcc aga att aca aaa ttt ttt caa gaa caa cca ctg gag   517
Val Glu Tyr Ser Arg Ile Thr Lys Phe Phe Gln Glu Gln Pro Leu Glu
                100                 105                 110

gga tat acc ctt ttc tct cac agg tct gcg cct aat gga ttc aaa gtt   565
Gly Tyr Thr Leu Phe Ser His Arg Ser Ala Pro Asn Gly Phe Lys Val
            115                 120                 125

gct ata gta cta agt gaa ctt gga ttt cat tat aac aca atc ttc cta   613
Ala Ile Val Leu Ser Glu Leu Gly Phe His Tyr Asn Thr Ile Phe Leu
    130                 135                 140

gat ttc aat ctt ggc gaa cat agg gcc ccc gaa ttt gtg tct gtg aac   661
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-7-

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Asp Phe Asn Leu Gly Glu His Arg Ala Pro Glu Phe Val Ser Val Asn
145             150             155             160

cct aat gca aga gtt cca gct tta atc gat cat ggt atg gac aac ttg    709
Pro Asn Ala Arg Val Pro Ala Leu Ile Asp His Gly Met Asp Asn Leu
                165             170             175

tct att tgg gaa tca ggg gcg att tta tta cat ttg gta aat aaa tat    757
Ser Ile Trp Glu Ser Gly Ala Ile Leu Leu His Leu Val Asn Lys Tyr
            180             185             190   .

tac aaa gag act ggt aat cca tta ctc tgg tcc gat gat tta gct gac    805
Tyr Lys Glu Thr Gly Asn Pro Leu Leu Trp Ser Asp Asp Leu Ala Asp
            195             200             205

caa tca caa atc aac gca tgg ttg ttc ttc caa acg tca ggg cat gcg    853
Gln Ser Gln Ile Asn Ala Trp Leu Phe Phe Gln Thr Ser Gly His Ala
        210             215             220

cca atg att gga caa gct tta cat ttc aga tac ttc cat tca caa aag    901
Pro Met Ile Gly Gln Ala Leu His Phe Arg Tyr Phe His Ser Gln Lys
225                 230             235             240

ata gca agt gct gta gaa aga tat acg gat gag gtt aga aga gtt tac    949
Ile Ala Ser Ala Val Glu Arg Tyr Thr Asp Glu Val Arg Arg Val Tyr
                245             250             255

ggt gta gtg gag atg gcc ttg gct gaa cgt aga gaa gcg ctg gtg atg    997
Gly Val Val Glu Met Ala Leu Ala Glu Arg Arg Glu Ala Leu Val Met
                260             265             270

gaa tta gac acg gaa aat gcg gct gca tac tca gct ggt aca aca cca   1045
Glu Leu Asp Thr Glu Asn Ala Ala Ala Tyr Ser Ala Gly Thr Thr Pro
            275             280             285

atg tca caa agt cgt ttc ttt gat tat ccc gta tgg ctt gta gga gat   1093
Met Ser Gln Ser Arg Phe Phe Asp Tyr Pro Val Trp Leu Val Gly Asp
        290             295             300

aaa tta act ata gca gat ttg gcc ttt gtc cca tgg aat aat gtc gtg   1141
Lys Leu Thr Ile Ala Asp Leu Ala Phe Val Pro Trp Asn Asn Val Val
305             310             315             320

gat aga att ggc att aat atc aaa att gaa ttt cca gaa gtt tac aaa   1189
Asp Arg Ile Gly Ile Asn Ile Lys Ile Glu Phe Pro Glu Val Tyr Lys
                325             330             335

tgg acg aag cat atg atg aga aga ccc gcg gtc atc aag gca ttg cgt   1237
Trp Thr Lys His Met Met Arg Arg Pro Ala Val Ile Lys Ala Leu Arg
            340             345             350

ggt gaa tga aggctgcttt aaaaacaaga aagaaagaag aaggaggaaa           1286
Gly Glu
        355

agaaggttat aagggtatgt ataggcag acaaaaagga aaattaagtg caaatataaa 1346

caaaaatgtc atagaagtat ataatagttt tgaaatttct gttgcttcta tttattcttt 1406

gttaccccaa ccacagaatt c                                          1427


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Arg Gln Val Asn Ile Gly Asn Arg Asn Ser Asn Thr Thr Thr Asp Gln
                20   25   30

Ser Asn Ile Asn Phe Glu Phe Ser Thr Gly Val Asn Asn Asn Asn Asn
        35   40   45

Asn Asn Ser Ser Ser Asn Asn Asn Asn Val Gln Asn Asn Asn Ser Gly
        50   55   60

Arg Asn Gly Ser Gln Asn Asn Asp Asn Glu Asn Asn Ile Lys Asn Thr
65   70   75   80

Leu Glu Gln His Arg Gln Gln Gln Gln Ala Phe Ser Asp Met Ser His
                85   90   95

Val Glu Tyr Ser Arg Ile Thr Lys Phe Phe Gln Glu Gln Pro Leu Glu
            100   105   110

Gly Tyr Thr Leu Phe Ser His Arg Ser Ala Pro Asn Gly Phe Lys Val
            115   120   125

Ala Ile Val Leu Ser Glu Leu Gly Phe His Tyr Asn Thr Ile Phe Leu
            130   135   140

Asp Phe Asn Leu Gly Glu His Arg Ala Pro Glu Phe Val Ser Val Asn
145   150   155   160

Pro Asn Ala Arg Val Pro Ala Leu Ile Asp His Gly Met Asp Asn Leu
                165   170   175

Ser Ile Trp Glu Ser Gly Ala Ile Leu Leu His Leu Val Asn Lys Tyr
                180   185   190

Tyr Lys Glu Thr Gly Asn Pro Leu Leu Trp Ser Asp Asp Leu Ala Asp
            195   200   205

Gln Ser Gln Ile Asn Ala Trp Leu Phe Phe Gln Thr Ser Gly His Ala
            210   215   220

Pro Met Ile Gly Gln Ala Leu His Phe Arg Tyr Phe His Ser Gln Lys
225   230   235   240

Ile Ala Ser Ala Val Glu Arg Tyr Thr Asp Glu Val Arg Arg Val Tyr
                245   250   255

Gly Val Val Glu Met Ala Leu Ala Glu Arg Arg Glu Ala Leu Val Met
            260   265   270

Glu Leu Asp Thr Glu Asn Ala Ala Ala Tyr Ser Ala Gly Thr Thr Pro
            275   280   285

Met Ser Gln Ser Arg Phe Phe Asp Tyr Pro Val Trp Leu Val Gly Asp
            290   295   300

Lys Leu Thr Ile Ala Asp Leu Ala Phe Val Pro Trp Asn Asn Val Val

Asp Arg Ile Gly Ile Asn Ile Lys Ile Glu Phe Pro Glu Val Tyr Lys
                325   330   335

Trp Thr Lys His Met Met Arg Arg Pro Ala Val Ile Lys Ala Leu Arg
                340   345   350

Gly Glu

<210> 5
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<220>
<223> Description of Artificial Sequence: FLAG peptide

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Asp Tyr Lys Asp Asp Asp Asp Lys
  1   5

<210> 6
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Asp Tyr Lys Asp Glu Asp Asp Lys
  1   5

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<213> Artificial Sequence

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  1   5   10

<210> 9
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Glu Gln Lys Leu Leu Ser Glu Glu Asp Leu Asn
  1   5   10

<210> 10
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<212> PRT
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<400> 10
Pro Gln Gly Gly Tyr Gln Gln Tyr Asn
  1   5

<210> 11
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ccattaccga catttgggcg ctatacgtgc atatgttcat gtatgtatct gtatttaaaa 60

cacttttgta ttattttcc tcatatatgt gtataggttt atacggatga tttaattatt 120

acttcaccac cctttatttc aggctgatat cttagccttg ttactagtta gaaaaagaca 180

tttttgctgt cagtcactgt caagagattc ttttgctggc atttcttcta gaagcaaaaa 240

gagcgatgcg tcttttccgc tgaaccgttc cagcaaaaaa gactaccaac gcaatatgga 300

ttgtcagaat catataaaag agaagcaaat aactccttgt cttgtatcaa ttgcattata 360

atatcttctt gttagtgcaa tatcatatag aagtcatcga aatagatatt aagaaaaaca 420

aactgtacaa tcaatcaatc aatca   445

<210> 12
<211> 717
<212> DNA
<213> Aequorea victoria

<400> 12
atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60

gatgttaatg gtcacaaatt ttctgtctcc ggtgaaggtg aaggtgatgc tacttacggt 120

aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180

gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240

- 11 -

```
catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300

aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaaggtga taccttagtt 360

aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420

ttggaataca actataactc tcacaatgtt tacatcatgg ctgacaaaca aagaatggt 480

atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540

cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600

ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggtcttg 660

ttagaatttg ttactgctgc tggtattacc catggtatgg atgaattgta caaataa      717
```

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HA
      tag-encoding sequence

<400> 13
tacccatacg acgtcccaga ctacgct   27

<210> 14
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: yeast
      Sup35Rdelta2-5 encoding sequence

<220>
<221> CDS
<222> (1)..(645)

<400> 14
```
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac    48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
 1               5                  10                  15

agc cag aac ggt aac caa caa caa ggt aac aac aga tac caa ggt tat    96
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
                20                  25                  30

caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat   144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
            35                  40                  45

tac caa ggt tat tct ggg tac cca caa ggt ggc cgt gga aat tac aaa   192
Tyr Gln Gly Tyr Ser Gly Tyr Pro Gln Gly Gly Arg Gly Asn Tyr Lys
        50                  55                  60

aac ttc aac tac aat aac aat ttg caa gga tat caa gct ggt ttc caa   240
Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln
 65                  70                  75                  80
```

```
cca cag tct caa ggt atg tct ttg aac gac ttt caa aag caa caa aag    288
Pro Gln Ser Gln Gly Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys
                85                  90                  95

cag gcc gct ccc aaa cca aag aag act ttg aag ctt gtc tcc agt tcc    336
Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser
            100                 105                 110

ggt atc aag ttg gcc aat gct acc aag aag gtt ggc aca aaa cct gcc    384
Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala
            115                 120                 125

gaa tct gat aag aaa gag gaa gag aag tct gct gaa acc aaa gaa cca    432
Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro
        130                 135                 140

act aaa gag cca aca aag gtc gaa gaa cca gtt aaa aag gag gag aaa    480
Thr Lys Glu Pro Thr Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys
145                 150                 155                 160

cca gtc cag act gaa gaa aag acg gag gaa aaa tcg gaa ctt cca aag    528
Pro Val Gln Thr Glu Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys
                165                 170                 175

gta gaa gac ctt aaa atc tct gaa tca aca cat aat acc aac aat gcc    576
Val Glu Asp Leu Lys Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala
            180                 185                 190

aat gtt acc agt gct gat gcc ttg atc aag gaa cag gaa gaa gaa gtg    624
Asn Val Thr Ser Ala Asp Ala Leu Ile Lys Glu Gln Glu Glu Glu Val
            195                 200                 205

gat gac gaa gtt gtt aac gat                                        645
Asp Asp Glu Val Val Asn Asp
    210                 215


<210> 15
<211> 215
<212> PRT
<213> Artificial Sequence

<400> 15
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
  1               5                  10                  15

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
              20                  25                  30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
            35                  40                  45

Tyr Gln Gly Tyr Ser Gly Tyr Pro Gln Gly Gly Arg Gly Asn Tyr Lys
        50                  55                  60

Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln
 65                  70                  75                  80

Pro Gln Ser Gln Gly Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys
                85                  90                  95

Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser
            100                 105                 110
```

```
Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala
        115             120             125

Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro
        130             135             140

Thr Lys Glu Pro Thr Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys
145             150             155             160

Pro Val Gln Thr Glu Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys
                165             170             175

Val Glu Asp Leu Lys Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala
            180             185             190

Asn Val Thr Ser Ala Asp Ala Leu Ile Lys Glu Gln Glu Glu Glu Val
        195             200             205

Asp Asp Glu Val Val Asn Asp
    210             215
```

<210> 16
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: yeast
      Sup35R2E2 encoding sequence

<220>
<221> CDS
<222> (1)..(813)

<400> 16
```
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac      48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
 1               5                  10                  15

agc cag aac ggt aac caa caa caa ggt aac aac aga tac caa ggt tat      96
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
                20                  25                  30

caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat     144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
            35                  40                  45

tac caa ggt tat tct ggg tac caa caa ggt ggc tat caa cag tac aat     192
Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
        50                  55                  60

ccc caa ggt ggc tat caa cag tac aat ccc caa ggt ggc tat caa cag     240
Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln
 65                  70                  75                  80

tac aat ccc gac gcc ggt tac cag caa cag tat aat cct caa gga ggc     288
Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly
                85                  90                  95

tat caa cag tac aat cct caa ggc ggt tat cag cag caa ttc aat cca     336
Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro
                100                 105                 110
```

- 14 -

```
caa ggt ggc cgt gga aat tac aaa aac ttc aac tac aat aac aat ttg      384
Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu
        115             120             125

caa gga tat caa gct ggt ttc caa cca cag tct caa ggt atg tct ttg      432
Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu
        130             135             140

aac gac ttt caa aag caa caa aag cag gcc gct ccc aaa cca aag aag      480
Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys
145             150             155             160

act ttg aag ctt gtc tcc agt tcc ggt atc aag ttg gcc aat gct acc      528
Thr Leu Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr
                165             170             175

aag aag gtt ggc aca aaa cct gcc gaa tct gat aag aaa gag gaa gag      576
Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu
            180             185             190

aag tct gct gaa acc aaa gaa cca act aaa gag cca aca aag gtc gaa      624
Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu
            195             200             205

gaa cca gtt aaa aag gag gag aaa cca gtc cag act gaa gaa aag acg      672
Glu Pro Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr
        210             215             220

gag gaa aaa tcg gaa ctt cca aag gta gaa gac ctt aaa atc tct gaa      720
Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu
225             230             235             240

tca aca cat aat acc aac aat gcc aat gtt acc agt gct gat gcc ttg      768
Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu
                245             250             255

atc aag gaa cag gaa gaa gaa gtg gat gac gaa gtt gtt aac gat          813
Ile Lys Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp
        260             265             270
```

<210> 17
<211> 271
<212> PRT
<213> Artificial Sequence

<400> 17
```
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
 1               5               10              15

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
            20              25              30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
            35              40              45

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
    50              55              60

Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln
65              70              75              80

Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly
```

```
                    85                      90                      95
Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro
            100                     105                     110

Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu
            115                     120                     125

Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu
            130                     135                     140

Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys
145                     150                     155                     160

Thr Leu Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr
                165                     170                     175

Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu
            180                     185                     190

Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu
            195                     200                     205

Glu Pro Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr
            210                     215                     220

Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu
225                     230                     235                     240

Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu
                245                     250                     255

Ile Lys Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp
            260                     265                     270


<210> 18
<211> 641
<212> DNA
<213> MOUSE

<220>
<221> CDS
<222> (1)..(633)

<400> 18
atg tct aaa aag cgg cca aag cct gga ggg tgg aac acc ggt gga agc    48
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
 1               5                   10                  15

cgg tat ccc ggg cag gga agc cct gga ggc aac cgt tac cca cct cag    96
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
                20                  25                  30

ggt ggc acc tgg ggg cag ccc cac ggt ggt ggc tgg gga caa ccc cat   144
Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His
            35                  40                  45

ggg ggc agc tgg gga caa cct cat ggt ggt agt tgg ggt cag ccc cat   192
Gly Gly Ser Trp Gly Gln Pro His Gly Gly Ser Trp Gly Gln Pro His
        50                  55                  60

ggc ggt gga tgg ggc caa gga ggg ggt acc cat aat cag tgg aac aag   240
```

- 16 -

```
Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn Lys
 65              70              75                  80

ccc agc aaa cca aaa acc aac ctc aag cat gtg gca ggg gct gcg gca    288
Pro Ser Lys Pro Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala
                 85              90                  95

gct ggg gca gta gtg ggg ggc ctt ggt ggc tac atg ctg ggg agc gcc    336
Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala
            100             105             110

gtg agc agg ccc atg atc cat ttt ggc aac gac tgg gag gac cgc tac    384
Val Ser Arg Pro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr
        115             120             125

tac cgt gaa aac atg tac cgc tac cct aac caa gtg tac tac agg cca    432
Tyr Arg Glu Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro
    130             135             140

gtg gat cag tac agc aac cag aac aac ttc gtg cac gac tgc gtc aat    480
Val Asp Gln Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Val Asn
145             150             155             160

atc acc atc aag cag cac acg gtc acc acc acc acc aag ggg gag aac    528
Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu Asn
            165             170             175

ttc acc gag acc gat gtg aag atg atg gag cgc gtg gtg gag cag atg    576
Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met
            180             185             190

tgc gtc acc cag tac cag aag gag tcc cag gcc tat tac gac ggg aga    624
Cys Val Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg
        195             200             205

aga tcc agc tgataacc                                               641
Arg Ser Ser
    210


<210> 19
<211> 211
<212> PRT
<213> MOUSE

<400> 19
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
 1               5               10                  15

Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
            20              25              30

Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His
        35              40              45

Gly Gly Ser Trp Gly Gln Pro His Gly Gly Ser Trp Gly Gln Pro His
    50              55              60

Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn Lys
 65              70              75                  80

Pro Ser Lys Pro Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala
                 85              90                  95
```

```
Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala
            100             105             110

Val Ser Arg Pro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr
            115             120             125

Tyr Arg Glu Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro
        130             135             140

Val Asp Gln Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Val Asn
145             150             155             160

Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Lys Gly Glu Asn
                165             170             175

Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met
            180             185             190

Cys Val Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg
            195             200             205

Arg Ser Ser
    210
```

<210> 20
<211> 644
<212> DNA
<213> Mesocricetus auratus

<220>
<221> CDS
<222> (1)..(636)

<400> 20
```
atg tct aag aag cgg cca aag cct gga ggg tgg aac act ggc gga agc   48
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
  1           5                  10                  15

cga tac cct ggg cag ggc agc cct gga ggc aac cgt tac cca cct cag   96
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
                20                  25                  30

ggt ggc ggc aca tgg ggg caa ccc cat ggt ggt ggc tgg gga cag ccc  144
Gly Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
            35                  40                  45

cat ggt ggt ggc tgg gga cag ccc cat ggt ggt ggc tgg ggt cag ccc  192
His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
        50                  55                  60

cat ggt ggt ggc tgg ggt caa gga ggt ggc acc cac aat cag tgg aac  240
His Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn
 65                  70                  75                  80

aag ccc agt aag cca aaa acc aac atg aag cac atg gcc ggc gct gct  288
Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met Ala Gly Ala Ala
                85                  90                  95

gcg gca ggg gcc gtg gtg ggg ggc ctt ggt ggc tac atg ctg ggg agt  336
Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser
            100                 105                 110
```

- 18 -

```
gcc atg agc agg ccc atg atg cat ttt ggc aat gac tgg gag gac cgc    384
Ala Met Ser Arg Pro Met Met His Phe Gly Asn Asp Trp Glu Asp Arg
        115             120                 125

tac tac cgt gaa aac atg aac cgc tac cct aac caa gtg tat tac cgg    432
Tyr Tyr Arg Glu Asn Met Asn Arg Tyr Pro Asn Gln Val Tyr Tyr Arg
        130             135                 140

cca gtg gac cag tac aac aac cag aac aac ttt gtg cac gat tgt gtc    480
Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val
145                 150                 155                 160

aac atc acc atc aag cag cac aca gtc acc acc acc acc aag ggg gag    528
Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu
                165                 170                 175

aac ttc acg gag acc gac atc aag ata atg gag cgc gtg gtg gag cag    576
Asn Phe Thr Glu Thr Asp Ile Lys Ile Met Glu Arg Val Val Glu Gln
            180                 185                 190

atg tgt acc acc cag tat cag aag gag tcc cag gcc tac tac gat gga    624
Met Cys Thr Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly
        195                 200                 205

aga agg tcc agc tgataacc                                           644
Arg Arg Ser Ser
        210


<210> 21
<211> 212
<212> PRT
<213> Mesocricetus auratus

<400> 21
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
  1               5                   10                  15

Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
                20                  25                  30

Gly Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
            35                  40                  45

His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
        50                  55                  60

His Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn
65                  70                  75                  80

Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met Ala Gly Ala Ala
                85                  90                  95

Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser
            100                 105                 110

Ala Met Ser Arg Pro Met Met His Phe Gly Asn Asp Trp Glu Asp Arg
        115                 120                 125

Tyr Tyr Arg Glu Asn Met Asn Arg Tyr Pro Asn Gln Val Tyr Tyr Arg
        130                 135                 140

Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val
```

- 19 -

Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu
            165   170   175

Asn Phe Thr Glu Thr Asp Ile Lys Ile Met Glu Arg Val Val Glu Gln
            180   185   190

Met Cys Thr Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly
            195   200   205

Arg Arg Ser Ser
        210

<210> 22
<211> 780
<212> PRT
<213> Saccharomyces cerevisiae

<400> 22
Met Lys Lys Lys Asp Asn Ser Asp Asp Lys Asp Asn Val Ala Ser Gly
    1   5   10   15

Gly Tyr Lys Asn Ala Ala Asp Ala Gly Ser Asn Asn Ala Ser Lys Lys
            20   25   30

Ser Ser Tyr Arg Asn Trp Lys Gly Gly Asn Tyr Gly Gly Tyr Ser Tyr
            35   40   45

Asn Ser Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr
        50   55   60

Asn Asn Tyr Asn Asn Tyr Asn Lys Tyr Asn Gly Gly Tyr Lys Ser Thr
 65   70   75   80

Tyr Lys Ser Ala Val Thr Asn Ser Gly Thr Thr Ser Ala Ser Thr Thr
                85   90   95

Ser Thr Ser Asn Lys Ser Asn Thr Ser Ser Lys Cys Ser Thr Asp Cys
            100   105   110

Lys Asn Lys Gly Lys Gly Asn Ser Thr Gly Lys Trp Lys Val Asp Val
            115   120   125

Ser Lys Lys Lys Asn Ser Val Arg Ser Ala Met Ser Asn Ala Ser Gly
            130   135   140

Lys Ala Tyr Asn Val Ala Asp Cys Ser Asp Lys Asn Thr Val Lys Arg
145   150   155   160

Ala Ala His Ala Asp Ser Asn Cys Met Ala Thr Cys Val Thr Asp Tyr
                165   170   175

Ser Ser Gly Ala Lys Trp Ala Lys Met Ala Ala Ser Val Val Asp Arg
            180   185   190

Arg Asp Ser Ala Asn Asp Thr Lys Asp Ala Val Val Thr Asp Val Ala
            195   200   205

Thr Asp Lys Ala Lys Gly Tyr Lys Thr Asp Tyr Val Ser Asp Asn Asp
    210   215   220

- 20 -

```
Ser Arg Tyr Lys Val Asp Thr Asp Ser Lys Val Ser Val Lys Ser Ser
225             230             235             240

Ser Val Thr Val Ala Val Thr Ser Ser Val Asn Arg Ser Asn Ser Ser
            245             250             255

Ser Ser Arg Thr Val Val Val Asn Thr Arg Val Asn Asn Arg Asn Ser
        260             265             270

Gly Lys Val Val Asp Thr Ala Ser Val Arg Ala Lys Ala Asn Val Lys
        275             280             285

Asp Asp Ala Asp Lys Asn Lys Ser Gly Arg Thr Gly Arg Asp Asp His
    290             295             300

Lys Asp Lys Ala Asp Asp Ser Cys Val Lys Tyr Met Asn Asp Thr Val
305             310             315             320

Lys Tyr Met Ser Lys Thr Val Asp Ser Asn Val Asn Asp Trp Lys Arg
            325             330             335

Asp Thr Ala Val Gly Gly Ser Asp Ser Arg Val Lys Asp His Asn Arg
            340             345             350

Ala Tyr Lys Arg Ala Asp Asp Gly Val Asn Thr Asp Ser Ala Tyr Gly
        355             360             365

Ser Arg Met Asn Lys Thr Asn Arg Lys Gly His Arg Tyr Gly Cys Gly
    370             375             380

Arg Asn Gly Ala Gly Lys Ser Thr Met Arg Ala Ala Asn Gly Asp Gly
385             390             395             400

Asp Lys Asp Thr Arg Thr Cys Val His Lys Gly Gly Asp Asp Val Ser
            405             410             415

Ala Asp Ser Thr Ser Arg Ala Ala Ala Ser Val Gly Asp Arg Arg Ala
        420             425             430

Thr Val Gly Ser Ser Gly Gly Trp Lys Met Lys Ala Arg Ala Met Lys
        435             440             445

Ala Asp Asp Thr Asn His Asp Val Ser Asn Val Lys Trp Tyr His Thr
    450             455             460

Asp Thr Ser Val Ser His Asp Ser Gly Asp Thr Val Cys Thr Asp His
465             470             475             480

Tyr Asn Lys Lys Ala Tyr Tyr Lys Gly Asn Ala Ala Val Lys Ala Lys
            485             490             495

Ser Tyr Tyr Thr Thr Asp Ser Asn Ala Met Arg Gly Thr Gly Val Lys
        500             505             510

Ser Asn Thr Arg Ala Val Ala Lys Met Thr Asp Val Thr Ser Tyr Gly
        515             520             525

Ala Lys Ser Ser His Val Ser Cys Ser Ser Ser Ser Arg Val Ala Cys
    530             535             540

Gly Asn Gly Ala Gly Lys Ser Thr Lys Thr Gly Val Asn Gly Lys Val
545             550             555             560
```

Lys His Asn Arg Gly Tyr Ala His Ala His Val Asn His Lys Lys Thr
                565   570   575

Ala Asn Tyr Trp Arg Tyr Gly Asp Asp Arg Val Lys Ser Arg Lys Ser
            580   585   590

Asp Lys Met Met Thr Lys Asp Asp Asp Gly Arg Gly Lys Arg Ala Ala
        595   600   605

Val Gly Arg Lys Lys Lys Ser Tyr Val Lys Trp Lys Tyr Trp Lys Lys
    610   615   620

Tyr Asn Ser Trp Val Lys Asp Val Val His Gly Lys Val Lys Asp Asp
625   630   635   640

His Ala Ser Arg Gly Gly Tyr Arg Ser Val Thr Lys His Asp Val Gly
            645   650   655

Asp Ser Ala Asn His Thr Gly Ser Ser Gly Gly Val Lys Val Val Ala
        660   665   670

Gly Ala Met Trp Asn Asn His Val Asp Thr Asn Tyr Asp Arg Asp Ser
    675   680   685

Gly Ala Ala Val Ala Arg Asp Trp Ser Gly Gly Val Val Met Ser His
    690   695   700

Asn Asn Val Gly Ala Cys Trp Val Asn Gly Lys Met Val Lys Gly Ser
705   710   715   720

Ala Val Asp Ser Lys Asp Gly Gly Asn Ala Asp Ala Val Gly Lys Ala
            725   730   735

Ser Asn Ala Lys Ser Val Asp Asp Asp Asp Ser Ala Asn Lys Val Lys
            740   745   750

Arg Lys Lys Arg Thr Arg Asn Lys Lys Ala Arg Arg Arg Arg Tyr Trp
            755   760   765

Ser Ser Lys Gly Thr Lys Val Asp Thr Asp Asp Asp
    770   775   780

<210> 23
<211> 1075
<212> PRT
<213> Saccharomyces cerevisiae

<400> 23
Met Asp Asn Lys Arg Leu Tyr Asn Gly Asn Leu Ser Asn Ile Pro Glu
  1   5   10   15

Val Ile Asp Pro Gly Ile Thr Ile Pro Ile Tyr Glu Glu Asp Ile Arg
            20   25   30

Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val Ser Asp
        35   40   45

Lys Arg Gly Arg Ser Ser Ser Thr Ser Pro Gln Lys Ile Gly Ser Tyr
    50   55   60

Arg Thr Arg Ala Gly Arg Phe Ser Asp Thr Leu Thr Asn Leu Leu Pro
65   70   75   80

- 22 -

Ser Ile Ser Ala Lys Leu His His Ser Lys Lys Ser Thr Pro Val Val
                85   90   95

Val Val Pro Pro Thr Ser Ser Thr Pro Asp Ser Leu Asn Ser Thr Thr
            100   105   110

Tyr Ala Pro Arg Val Ser Ser Asp Ser Phe Thr Val Ala Thr Pro Leu
            115   120   125

Ser Leu Gln Ser Thr Thr Thr Arg Thr Arg Thr Arg Asn Asn Thr Val
    130   135   140

Ser Ser Gln Ile Thr Ala Ser Ser Ser Leu Thr Thr Asp Val Gly Asn
145   150   155   160

Ala Thr Ser Ala Asn Ile Trp Ser Ala Asn Ala Glu Ser Asn Thr Ser
            165   170   175

Ser Ser Pro Leu Phe Asp Tyr Pro Leu Ala Thr Ser Tyr Phe Glu Pro
            180   185   190

Leu Thr Arg Phe Lys Ser Thr Asp Asn Tyr Thr Leu Pro Gln Thr Ala
            195   200   205

Gln Leu Asn Ser Phe Leu Glu Lys Asn Gly Asn Pro Asn Ile Trp Ser
    210   215   220

Ser Ala Gly Asn Ser Asn Thr Asp His Leu Asn Thr Pro Ile Val Asn
225   230   235   240

Arg Gln Arg Ser Gln Ser Gln Ser Thr Thr Asn Arg Val Tyr Thr Asp
            245   250   255

Ala Pro Tyr Tyr Gln Gln Pro Ala Gln Asn Tyr Gln Val Gln Val Pro
            260   265   270

Pro Arg Val Pro Lys Ser Thr Ser Ile Ser Pro Val Ile Leu Asp Asp
            275   280   285

Val Asp Pro Ala Ser Ile Asn Trp Ile Thr Ala Asn Gln Lys Val Pro
    290   295   300

Leu Val Asn Gln Ile Ser Ala Leu Leu Pro Thr Asn Thr Ile Ser Ile
305   310   315   320

Ser Asn Val Phe Pro Leu Gln Pro Thr Gln Gln His Gln Gln Asn Ala
            325   330   335

Val Asn Leu Thr Ser Thr Ser Leu Ala Thr Leu Cys Ser Gln Tyr Gly
            340   345   350

Lys Val Leu Ser Ala Arg Thr Leu Arg Gly Leu Asn Met Ala Leu Val
            355   360   365

Glu Phe Ser Thr Val Glu Ser Ala Ile Cys Ala Leu Glu Ala Leu Gln
    370   375   380

Gly Lys Glu Leu Ser Lys Val Gly Ala Pro Ser Thr Val Ser Phe Ala
385   390   395   400

Arg Val Leu Pro Met Tyr Glu Gln Pro Leu Asn Val Asn Gly Phe Asn
            405   410   415

```
Asn Thr Pro Lys Gln Pro Leu Leu Gln Glu Gln Leu Asn His Gly Val
            420             425             430

Leu Asn Tyr Gln Leu Gln Gln Ser Leu Gln Gln Pro Glu Leu Gln Gln
            435             440             445

Gln Pro Thr Ser Phe Asn Gln Pro Asn Leu Thr Tyr Cys Asn Pro Thr
    450             455             460

Gln Asn Leu Ser His Leu Gln Leu Ser Ser Asn Glu Asn Glu Pro Tyr
465             470             475             480

Pro Phe Pro Leu Pro Pro Pro Ser Leu Ser Asp Ser Lys Lys Asp Ile
            485             490             495

Leu His Thr Ile Ser Ser Phe Lys Leu Glu Tyr Asp His Leu Glu Leu
            500             505             510

Asn His Leu Leu Gln Asn Ala Leu Lys Asn Lys Gly Val Ser Asp Thr
            515             520             525

Asn Tyr Phe Gly Pro Leu Pro Glu His Asn Ser Lys Val Pro Lys Arg
    530             535             540

Lys Asp Thr Phe Asp Ala Pro Lys Leu Arg Glu Leu Arg Lys Gln Phe
545             550             555             560

Asp Ser Asn Ser Leu Ser Thr Ile Glu Met Glu Gln Leu Ala Ile Val
            565             570             575

Met Leu Asp Gln Leu Pro Glu Leu Ser Ser Asp Tyr Leu Gly Asn Thr
            580             585             590

Val Ile Gln Lys Leu Phe Glu Asn Ser Ser Asn Ile Ile Arg Asp Ile
    595             600             605

Met Leu Arg Lys Cys Asn Lys Tyr Leu Thr Ser Met Gly Val His Lys
    610             615             620

Asn Gly Thr Trp Val Cys Gln Lys Ile Ile Lys Met Ala Asn Thr Pro
625             630             635             640

Arg Gln Ile Asn Leu Val Thr Ser Gly Val Ser Asp Tyr Cys Thr Pro
            645             650             655

Leu Phe Asn Asp Gln Phe Gly Asn Tyr Val Ile Gln Gly Ile Leu Lys
            660             665             670

Phe Gly Phe Pro Trp Asn Ser Phe Ile Phe Glu Ser Val Leu Ser His
            675             680             685

Phe Trp Thr Ile Val Gln Asn Arg Tyr Gly Ser Arg Ala Val Arg Ala
    690             695             700

Cys Leu Glu Ala Asp Ser Ile Ile Thr Gln Cys Gln Leu Leu Thr Ile
705             710             715             720

Thr Ser Leu Ile Ile Val Leu Ser Pro Tyr Leu Ala Thr Asp Thr Asn
            725             730             735

Gly Thr Leu Leu Ile Thr Trp Leu Leu Asp Thr Cys Thr Leu Pro Asn
            740             745             750
```

- 24 -

```
Lys Asn Leu Ile Leu Cys Asp Lys Leu Val Asn Lys Asn Leu Val Lys
        755                 760                 765

Leu Cys Cys His Lys Leu Gly Ser Leu Thr Val Leu Lys Ile Leu Asn
        770                 775                 780

Leu Arg Gly Gly Glu Glu Glu Ala Leu Ser Lys Asn Lys Ile Ile His
785                     790                 795                 800

Ala Ile Phe Asp Gly Pro Ile Ser Ser Asp Ser Ile Leu Phe Gln Ile
                805                 810                 815

Leu Asp Glu Gly Asn Tyr Gly Pro Thr Phe Ile Tyr Lys Val Leu Thr
            820                 825                 830

Ser Arg Ile Leu Asp Asn Ser Val Arg Asp Glu Ala Ile Thr Lys Ile
        835                 840                 845

Arg Gln Leu Ile Leu Asn Ser Asn Ile Asn Leu Gln Ser Arg Gln Leu
    850                 855                 860

Leu Glu Glu Val Gly Leu Ser Ser Ala Gly Ile Ser Pro Lys Gln Ser
865                     870                 875                 880

Ser Lys Asn His Arg Lys Gln His Pro Gln Gly Phe His Ser Pro Gly
            885                 890                 895

Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser Ser Asn Ser Arg
            900                 905                 910

His Asn Ser Val Ile Gln Met Asn Asn Ala Gly Pro Thr Pro Ala Leu
        915                 920                 925

Asn Phe Asn Pro Ala Pro Met Ser Glu Ile Asn Ser Tyr Phe Asn Asn
    930                 935                 940

Gln Gln Val Val Tyr Ser Gly Asn Gln Asn Gln Asn Gln Asn Gly Asn
945                 950                 955                 960

Ser Asn Gly Leu Asp Glu Leu Asn Ser Gln Phe Asp Ser Phe Arg Ile
            965                 970                 975

Ala Asn Gly Thr Asn Leu Ser Leu Pro Ile Val Asn Leu Pro Asn Val
            980                 985                 990

Ser Asn Asn Asn Asn Asn Tyr Asn Asn Ser Gly Tyr Ser Ser Gln Met
        995                 1000                1005

Asn Pro Leu Ser Arg Ser Val Ser His Asn Asn Asn Asn Asn Thr Asn
    1010                1015                1020

Asn Tyr Asn Asn Asn Asp Asn Asp Asn Asn Asn Asn Asn Asn Asn Asn
1025                1030                1035                1040

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
            1045                1050                1055

Ser Asn Asn Asn Asn Asn Asn Asp Thr Ser Leu Tyr Arg Tyr Arg Ser
        1060                1065                1070

Tyr Gly Tyr
        1075
```

<210> 24
<211> 76
<212> PRT
<213> Saccharomyces cerevisiae

<400> 24
Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Lys Ser Tyr Ser
1   5   10   15

Arg Ser Asn Ser Ser Ala His Asn Lys Thr Arg Gly Tyr Tyr Tyr His
            20   25   30

Gly Tyr Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn
        35   40   45

Gly Tyr Asn Gly Tyr Asn Gly His Val Tyr Val Arg Gly Asn Gly Cys
    50   55   60

Ala Ala Cys Ala Ala Cys Cys Cys Thr Met Asp Met
65   70   75

<210> 25
<211> 380
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25
Met Ser Ser Asp Asp Asn Asp Tyr Gly Asp Asp Lys Thr Thr Thr Val
1   5   10   15

Lys Lys Asn Lys Ala Gly Ser Gly Thr Ser Asp Ala Ala Ala Ser Ser
            20   25   30

Ser Asn Lys Asn Asn Asn Ser Asn Asn Ser Ser Ser Asn Asn Ser Asn
        35   40   45

Asp Thr Ser Ser Ser Lys Asp Gly Thr Ala Asn Asp Lys Gly Ser Asn
    50   55   60

Asp Thr Lys Asn Lys Lys Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn
65   70   75   80

Ala Ser Ser Ala Gly Ser Gly Trp Thr Met Ser Ser Ser Ser Val Thr
                85   90   95

Thr Lys Arg Ser Lys Ala Asp Ser Lys Ser Cys Lys Met Gly Gly Asn
            100   105   110

Trp Asp Thr Thr Asp Asn Arg Tyr Gly Lys Tyr Gly Thr Val Thr Asp
            115   120   125

Lys Met Lys Asp Ala Thr Gly Arg Ser Arg Gly Gly Ser Lys Ser Ser
    130   135   140

Val Asp Val Val Lys Thr His Asp Gly Lys Val Asp Lys Arg Ala Arg
145   150   155   160

Asp Asp Lys Thr Gly Lys Val Gly Gly Gly Asp Val Arg Lys Ser Trp
            165   170   175

Gly Thr Asp Ala Met Asp Lys Asp Thr Gly Ser Arg Gly Gly Val Thr
            180   185   190

```
Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Asn Lys Asp Lys Asp
        195             200             205
```

```
Arg Lys Lys Arg Ala Arg His Met Lys Ser Ser Asn Asn Gly Gly Asn
    210             215             220
```

```
Asn Gly Gly Asn Asn Met Asn Arg Arg Gly Gly Asn Gly Asn Gly Asp
225             230             235             240
```

```
Asn Met Tyr Asn Met Met Gly Gly Tyr Asn Met Met Asn Ala Met Thr
            245             250             255
```

```
Asp Tyr Tyr Lys Met Tyr Tyr Met Lys Thr Gly Met Asp Tyr Thr Met
            260             265             270
```

```
Tyr Met Met Ala Met Met Met Gly Ala Met Asn Ala Met Thr Asn Asp
        275             280             285
```

```
Ser Asn Ala Thr Gly Ser Ala Ser Asp Ser Asp Asn Asn Lys Ser Asn
    290             295             300
```

```
Asp Val Thr Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Asn Asn Gly
305             310             315             320
```

```
Lys Gly Ser Tyr Asn Asp Asp His Asn Ser Gly Tyr Gly Tyr Asn Arg
            325             330             335
```

```
Asp Arg Gly Asp Arg Asp Arg Asn Asp Arg Asp Arg Asp Tyr Asn His
            340             345             350
```

```
Arg Ser Gly Gly Asn His Arg Arg Asn Gly Arg Gly Gly Arg Gly Gly
            355             360             365
```

```
Tyr Asn Arg Arg Asn Asn Gly Tyr His Tyr Asn Arg
    370             375             380
```

```
<210> 26
<211> 256
<212> PRT
<213> Saccharomyces cerevisiae
```

```
<400> 26
Met Ser Ala Thr His Val Ser Val Val Asp Ala Val His Ala Asp Ala
  1             5               10              15
```

```
Val Ser Ala Ser Ala Ala Asn Asp Val Ser Asn Ala Tyr Gly Ser His
            20              25              30
```

```
Ser Val Asp Tyr Ala His His His Tyr Tyr Gly His Met His Gly Arg
        35              40              45
```

```
Met His His Arg Gly Ser Asn Thr Arg Val Arg Asp Val Ser Asn Gly
    50              55              60
```

```
Gly Met Lys Val Lys Asn Gly Ala Val Ala Ser Ala Ala Lys Ala Val
 65             70              75              80
```

```
His Gly Lys Ser Ala Asn Val Val Tyr Ser Lys Ala Lys Arg Tyr Arg
                85              90              95
```

```
Thr Met Lys Asn Gly Cys Ser Trp Asp Lys Asp Ala Arg Asn Ser Thr
            100             105             110
```

```
Thr Ser Ser Val Asn Thr Arg Asp Asp Gly Thr Gly Ala Ser Val Ala
        115                 120                 125

Arg Asn Asn Arg Gly Ser Val Thr Val Arg Asp Asp Asn Arg Arg Ser
        130                 135                 140

Asn Arg Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg
145                     150                 155                 160

Gly Gly Ser Arg Gly Gly Gly Gly Arg Gly Gly Gly Arg Gly Gly
                165                 170                 175

Tyr Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Tyr Ser Arg Gly Gly
            180                 185                 190

Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Ser Arg Gly Gly Tyr Asp Ser
            195                 200                 205

Arg Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Arg Asn Asp Tyr Gly
    210                 215                 220

Arg Gly Ser Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Gly Arg Gly Asp
225                     230                 235                 240

Tyr Gly Arg Asp Ala Tyr Arg Thr Arg Asp Ala Arg Arg Ser Thr Arg
            245                 250                 255
```

<210> 27
<211> 286
<212> PRT
<213> Saccharomyces cerevisiae

<400> 27
```
Met Ser Asp Ile Glu Glu Gly Thr Pro Thr Asn Asn Gly Gln Gln Lys
  1               5                  10                  15

Glu Arg Arg Lys Ile Glu Ile Lys Phe Ile Glu Asn Lys Thr Arg Arg
            20                  25                  30

His Val Thr Phe Ser Lys Arg Lys His Gly Ile Met Lys Lys Ala Phe
        35                  40                  45

Glu Leu Ser Val Leu Thr Gly Thr Gln Val Leu Leu Leu Val Val Ser
    50                  55                  60

Glu Thr Gly Leu Val Tyr Thr Phe Ser Thr Pro Lys Phe Glu Pro Ile
65                  70                  75                  80

Val Thr Gln Gln Glu Gly Arg Asn Leu Ile Gln Ala Cys Leu Asn Ala
                85                  90                  95

Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Asp Gly Asp Asp Asp Asp
            100                 105                 110

Asp Asp Asp Asp Asp Gly Asn Asp Met Gln Arg Gln Gln Pro Gln Gln
        115                 120                 125

Gln Gln Pro Gln Gln Gln Gln Gln Val Leu Asn Ala His Ala Asn Ser
    130                 135                 140
```

```
Leu Gly His Leu Asn Gln Asp Gln Val Pro Ala Gly Ala Leu Lys Gln
145                 150                 155                 160

Glu Val Lys Ser Gln Leu Leu Gly Gly Ala Asn Pro Asn Gln Asn Ser
                165                 170                 175

Met Ile Gln Gln Gln Gln His His Thr Gln Asn Ser Gln Pro Gln Gln
                180                 185                 190

Gln Gln Gln Gln Gln Pro Gln Gln Gln Met Ser Gln Gln Gln Met Ser
                195                 200                 205

Gln His Pro Arg Pro Gln Gln Gly Ile Pro His Pro Gln Gln Ser Gln
        210             215             220

Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln
225                 230                 235                 240

Gln Gln Gln Gln Gln Pro Leu Thr Gly Ile His Gln Pro His Gln Gln
                245             250             255

Ala Phe Ala Asn Ala Ala Ser Pro Tyr Leu Asn Ala Glu Gln Asn Ala
                260             265             270

Ala Tyr Gln Gln Tyr Phe Gln Glu Pro Gln Gln Gly Gln Tyr
                275             280             285


<210> 28
<211> 414
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28
Met Ala Lys Thr Thr Lys Val Lys Gly Asn Lys Lys Glu Val Lys Ala
  1           5               10              15

Ser Lys Gln Ala Lys Glu Glu Lys Ala Lys Ala Val Ser Ser Ser Ser
            20              25              30

Ser Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Glu Ser Glu
        35              40              45

Ser Glu Ser Glu Ser Glu Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser
    50              55                  60

Glu Ser Ser Ser Ser Ser Ser Ser Asp Ser Glu Ser Glu Ala Glu Thr
65              70              75              80

Lys Lys Glu Glu Ser Lys Asp Ser Ser Ser Ser Ser Asp Ser Ser
                85              90              95

Ser Asp Glu Glu Glu Glu Glu Glu Lys Glu Glu Thr Lys Lys Glu Glu
        100             105             110

Ser Lys Glu Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser Asp
        115             120             125

Ser Glu Ser Glu Lys Glu Glu Ser Asn Asp Lys Lys Arg Lys Ser Glu
        130             135             140

Asp Ala Glu Glu Glu Glu Asp Glu Glu Ser Ser Asn Lys Lys Gln Lys
145             150             155             160
```

Asn Glu Glu Thr Glu Glu Pro Ala Thr Ile Phe Val Gly Arg Leu Ser
                165   170   175

Trp Ser Ile Asp Asp Glu Trp Leu Lys Lys Glu Phe Glu His Ile Gly
                180   185   190

Gly Val Ile Gly Ala Arg Val Ile Tyr Glu Arg Gly Thr Asp Arg Ser
                195   200   205

Arg Gly Tyr Gly Tyr Val Asp Phe Glu Asn Lys Ser Tyr Ala Glu Lys
        210   215   220

Ala Ile Gln Glu Met Gln Gly Lys Glu Ile Asp Gly Arg Pro Ile Asn
225   230   235   240

Cys Asp Met Ser Thr Ser Lys Pro Ala Gly Asn Asn Asp Arg Ala Lys
                245   250   255

Lys Phe Gly Asp Thr Pro Ser Glu Pro Ser Asp Thr Leu Phe Leu Gly
            260   265   270

Asn Leu Ser Phe Asn Ala Asp Arg Asp Ala Ile Phe Glu Leu Phe Ala
            275   280   285

Lys His Gly Glu Val Val Ser Val Arg Ile Pro Thr His Pro Glu Thr
        290   295   300

Glu Gln Pro Lys Gly Phe Gly Tyr Val Gln Phe Ser Asn Met Glu Asp
305   310   315   320

Ala Lys Lys Ala Leu Asp Ala Leu Gln Gly Glu Tyr Ile Asp Asn Arg
                325   330   335

Pro Val Arg Leu Asp Phe Ser Ser Pro Arg Pro Asn Asn Asp Gly Gly
            340   345   350

Arg Gly Gly Ser Arg Gly Phe Gly Gly Arg Gly Gly Arg Gly Gly
            355   360   365

Asn Arg Gly Phe Gly Gly Arg Gly Gly Ala Arg Gly Gly Arg Gly Gly
        370   375   380

Phe Arg Pro Ser Gly Ser Gly Ala Asn Thr Ala Pro Leu Gly Arg Ser
385   390   395   400

Arg Asn Thr Ala Ser Phe Ala Gly Ser Lys Lys Thr Phe Asp
            405   410

<210> 29
<211> 405
<212> PRT
<213> Saccharomyces cerevisiae

<400> 29
Met Asp Thr Asp Lys Leu Ile Ser Glu Ala Glu Ser His Phe Ser Gln
  1   5   10   15

Gly Asn His Ala Glu Ala Val Ala Lys Leu Thr Ser Ala Ala Gln Ser
                20   25   30

Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
            35   40   45

- 30 -

```
Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
    50                      55                  60

Gln Asp Arg Ala Ala Gly Gly Gly Ser Ser Phe Met Asn Thr Leu Met
65                  70              75                          80

Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
                85                  90                      95

Leu Ala Thr Val Met Thr His Ser Ser Asn Lys Gly Ser Ser Asn Arg
            100             105             110

Gly Phe Asp Val Gly Thr Val Met Ser Met Leu Ser Gly Ser Gly Gly
        115             120             125

Gly Ser Gln Ser Met Gly Ala Ser Gly Leu Ala Ala Leu Ala Ser Gln
    130             135             140

Phe Phe Lys Ser Gly Asn Asn Ser Gln Gly Gln Gly Gln Gly Gln Gly
145             150                 155                         160

Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Ser Phe Thr Ala
            165             170             175

Leu Ala Ser Leu Ala Ser Ser Phe Met Asn Ser Asn Asn Asn Asn Gln
            180             185             190

Gln Gly Gln Asn Gln Ser Ser Gly Gly Ser Ser Phe Gly Ala Leu Ala
        195             200             205

Ser Met Ala Ser Ser Phe Met His Ser Asn Asn Asn Gln Asn Ser Asn
    210             215             220

Asn Ser Gln Gln Gly Tyr Asn Gln Ser Tyr Gln Asn Gly Asn Gln Asn
225             230             235                         240

Ser Gln Gly Tyr Asn Asn Gln Gln Tyr Gln Gly Gly Asn Gly Gly Tyr
            245             250             255

Gln Gln Gln Gln Gly Gln Ser Gly Gly Ala Phe Ser Ser Leu Ala Ser
        260             265             270

Met Ala Gln Ser Tyr Leu Gly Gly Gly Gln Thr Gln Ser Asn Gln Gln
    275             280             285

Gln Tyr Asn Gln Gln Gly Gln Asn Asn Gln Gln Gln Tyr Gln Gln Gln
    290             295             300

Gly Gln Asn Tyr Gln His Gln Gln Gln Gly Gln Gln Gln Gln Gly
305             310             315             320

His Ser Ser Ser Phe Ser Ala Leu Ala Ser Met Ala Ser Ser Tyr Leu
            325             330             335

Gly Asn Asn Ser Asn Ser Asn Ser Ser Tyr Gly Gly Gln Gln Gln Ala
            340             345             350

Asn Glu Tyr Gly Arg Pro Gln His Asn Gly Gln Gln Gln Ser Asn Glu
        355             360             365

Tyr Gly Arg Pro Gln Tyr Gly Gly Asn Gln Asn Ser Asn Gly Gln His
    370             375             380
```

- 31 -

```
Glu Ser Phe Asn Phe Ser Gly Asn Phe Ser Gln Gln Asn Asn Asn Gly
385                 390             395                 400

Asn Gln Asn Arg Tyr
                405


<210> 30
<211> 964
<212> PRT
<213> Saccharomyces cerevisiae

<400> 30
Met Pro Glu Gln Ala Gln Gln Gly Glu Gln Ser Val Lys Arg Arg Arg
  1           5               10              15

Val Thr Arg Ala Cys Asp Glu Cys Arg Lys Lys Val Lys Cys Asp
            20              25              30

Gly Gln Gln Pro Cys Ile His Cys Thr Val Tyr Ser Tyr Glu Cys Thr
        35              40              45

Tyr Lys Lys Pro Thr Lys Arg Thr Gln Asn Ser Gly Asn Ser Gly Val
    50              55                  60

Leu Thr Leu Gly Asn Val Thr Thr Gly Pro Ser Ser Ser Thr Val Val
 65                 70              75                  80

Ala Ala Ala Ala Ser Asn Pro Asn Lys Leu Leu Ser Asn Ile Lys Thr
                85              90                  95

Glu Arg Ala Ile Leu Pro Gly Ala Ser Thr Ile Pro Ala Ser Asn Asn
        100             105             110

Pro Ser Lys Pro Arg Lys Tyr Lys Thr Lys Ser Thr Arg Leu Gln Ser
        115             120             125

Lys Ile Asp Arg Tyr Lys Gln Ile Phe Asp Glu Val Phe Pro Gln Leu
    130             135             140

Pro Asp Ile Asp Asn Leu Asp Ile Pro Val Phe Leu Gln Ile Phe His
145             150             155             160

Asn Phe Lys Arg Asp Ser Gln Ser Phe Leu Asp Asp Thr Val Lys Glu
            165             170             175

Tyr Thr Leu Ile Val Asn Asp Ser Ser Ser Pro Ile Gln Pro Val Leu
        180             185             190

Ser Ser Asn Ser Lys Asn Ser Thr Pro Asp Glu Phe Leu Pro Asn Met
        195             200             205

Lys Ser Asp Ser Asn Ser Ala Ser Ser Asn Arg Glu Gln Asp Ser Val
    210             215             220

Asp Thr Tyr Ser Asn Ile Pro Val Gly Arg Glu Ile Lys Ile Ile Leu
225             230             235             240

Pro Pro Lys Ala Ile Ala Leu Gln Phe Val Lys Ser Thr Trp Glu His
            245             250             255

Cys Cys Val Leu Leu Arg Phe Tyr His Arg Pro Ser Phe Ile Arg Gln
            260             265             270
```

- 32 -

```
Leu Asp Glu Leu Tyr Glu Thr Asp Pro Asn Asn Tyr Thr Ser Lys Gln
        275             280             285

Met Gln Phe Leu Pro Leu Cys Tyr Ala Ala Ile Ala Val Gly Ala Leu
        290             295             300

Phe Ser Lys Ser Ile Val Ser Asn Asp Ser Ser Arg Glu Lys Phe Leu
305             310             315             320

Gln Asp Glu Gly Tyr Lys Tyr Phe Ile Ala Ala Arg Lys Leu Ile Asp
            325             330             335

Ile Thr Asn Ala Arg Asp Leu Asn Ser Ile Gln Ala Ile Leu Met Leu
        340             345             350

Ile Ile Phe Leu Gln Cys Ser Ala Arg Leu Ser Thr Cys Tyr Thr Tyr
        355             360             365

Ile Gly Val Ala Met Arg Ser Ala Leu Arg Ala Gly Phe His Arg Lys
    370             375             380

Leu Ser Pro Asn Ser Gly Phe Ser Pro Ile Glu Ile Glu Met Arg Lys
385             390             395             400

Arg Leu Phe Tyr Thr Ile Tyr Lys Leu Asp Val Tyr Ile Asn Ala Met
            405             410             415

Leu Gly Leu Pro Arg Ser Ile Ser Pro Asp Asp Phe Asp Gln Thr Leu
            420             425             430

Pro Leu Asp Leu Ser Asp Glu Asn Ile Thr Glu Val Ala Tyr Leu Pro
        435             440             445

Glu Asn Gln His Ser Val Leu Ser Ser Thr Gly Ile Ser Asn Glu His
    450             455             460

Thr Lys Leu Phe Leu Ile Leu Asn Glu Ile Ile Ser Glu Leu Tyr Pro
465             470             475             480

Ile Lys Lys Thr Ser Asn Ile Ile Ser His Glu Thr Val Thr Ser Leu
            485             490             495

Glu Leu Lys Leu Arg Asn Trp Leu Asp Ser Leu Pro Lys Glu Leu Ile
            500             505             510

Pro Asn Ala Glu Asn Ile Asp Pro Glu Tyr Glu Arg Ala Asn Arg Leu
        515             520             525

Leu His Leu Ser Phe Leu His Val Gln Ile Ile Leu Tyr Arg Pro Phe
        530             535             540

Ile His Tyr Leu Ser Arg Asn Met Asn Ala Glu Asn Val Asp Pro Leu
545             550             555             560

Cys Tyr Arg Arg Ala Arg Asn Ser Ile Ala Val Ala Arg Thr Val Ile
            565             570             575

Lys Leu Ala Lys Glu Met Val Ser Asn Asn Leu Leu Thr Gly Ser Tyr
            580             585             590

Trp Tyr Ala Cys Tyr Thr Ile Phe Tyr Ser Val Ala Gly Leu Leu Phe
            595             600             605
```

```
Tyr Ile His Glu Ala Gln Leu Pro Asp Lys Asp Ser Ala Arg Glu Tyr
    610             615             620

Tyr Asp Ile Leu Lys Asp Ala Glu Thr Gly Arg Ser Val Leu Ile Gln
625             630             635                 640

Leu Lys Asp Ser Ser Met Ala Ala Ser Arg Thr Tyr Asn Leu Leu Asn
            645             650             655

Gln Ile Phe Glu Lys Leu Asn Ser Lys Thr Ile Gln Leu Thr Ala Leu
        660             665             670

His Ser Ser Pro Ser Asn Glu Ser Ala Phe Leu Val Thr Asn Asn Ser
        675             680             685

Ser Ala Leu Lys Pro His Leu Gly Asp Ser Leu Gln Pro Pro Val Phe
    690             695             700

Phe Ser Ser Gln Asp Thr Lys Asn Ser Phe Ser Leu Ala Lys Ser Glu
705             710             715                 720

Glu Ser Thr Asn Asp Tyr Ala Met Ala Asn Tyr Leu Asn Asn Thr Pro
            725             730             735

Ile Ser Glu Asn Pro Leu Asn Glu Ala Gln Gln Gln Asp Gln Val Ser
            740             745             750

Gln Gly Thr Thr Asn Met Ser Asn Glu Arg Asp Pro Asn Asn Phe Leu
        755             760             765

Ser Ile Asp Ile Arg Leu Asp Asn Asn Gly Gln Ser Asn Ile Leu Asp
    770             775             780

Ala Thr Asp Asp Val Phe Ile Arg Asn Asp Gly Asp Ile Pro Thr Asn
785             790             795                 800

Ser Ala Phe Asp Phe Ser Ser Ser Lys Ser Asn Ala Ser Asn Asn Ser
            805             810             815

Asn Pro Asp Thr Ile Asn Asn Asn Tyr Asn Asn Val Ser Gly Lys Asn
            820             825             830

Asn Asn Asn Asn Asn Ile Thr Asn Asn Ser Asn Asn Asn His Asn Asn
        835             840             845

Asn Asn Asn Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
    850             855             860

Asn Asn Asn Asn Asn Ser Gly Asn Ser Ser Asn Asn Asn Asn Asn Asn
865             870             875                 880

Asn Asn Asn Lys Asn Asn Asn Asp Phe Gly Ile Lys Ile Asp Asn Asn
            885             890             895

Ser Pro Ser Tyr Glu Gly Phe Pro Gln Leu Gln Ile Pro Leu Ser Gln
            900             905             910

Asp Asn Leu Asn Ile Glu Asp Lys Glu Glu Met Ser Pro Asn Ile Glu
            915             920             925

Ile Lys Asn Glu Gln Asn Met Thr Asp Ser Asn Asp Ile Leu Gly Val
    930             935             940
```

```
Phe Asp Gln Leu Asp Ala Gln Leu Phe Gly Lys Tyr Leu Pro Leu Asn
945                 950             955                 960

Tyr Pro Ser Glu


<210> 31
<211> 758
<212> PRT
<213> Saccharomyces cerevisiae

<400> 31
Met Asp Asn Thr Thr Asn Ile Asn Thr Asn Glu Arg Ser Ser Asn Thr
 1               5                  10                  15

Asp Phe Ser Ser Ala Pro Asn Ile Lys Gly Leu Asn Ser His Thr Gln
                20              25                  30

Leu Gln Phe Asp Ala Asp Ser Arg Val Phe Val Ser Asp Val Met Ala
            35              40                  45

Lys Asn Ser Lys Gln Leu Leu Tyr Ala His Ile Tyr Asn Tyr Leu Ile
        50              55                  60

Lys Asn Asn Tyr Trp Asn Ser Ala Ala Lys Phe Leu Ser Glu Ala Asp
 65             70                  75                  80

Leu Pro Leu Ser Arg Ile Asn Gly Ser Ala Ser Gly Gly Lys Thr Ser
                85              90                  95

Leu Asn Ala Ser Leu Lys Gln Gly Leu Met Asp Ile Ala Ser Lys Gly
            100             105                 110

Asp Ile Val Ser Glu Asp Gly Leu Leu Pro Ser Lys Met Leu Met Asp
        115             120                 125

Ala Asn Asp Thr Phe Leu Leu Glu Trp Trp Glu Ile Phe Gln Ser Leu
    130             135                 140

Phe Asn Gly Asp Leu Glu Ser Gly Tyr Gln Gln Asp His Asn Pro Leu
145             150                 155                 160

Arg Glu Arg Ile Ile Pro Ile Leu Pro Ala Asn Ser Lys Ser Asn Met
                165                 170                 175

Pro Ser His Phe Ser Asn Leu Pro Pro Asn Val Ile Pro Pro Thr Gln
            180             185                 190

Asn Ser Phe Pro Val Ser Glu Glu Ser Phe Arg Pro Asn Gly Asp Gly
            195             200                 205

Ser Asn Phe Asn Leu Asn Asp Pro Thr Asn Arg Asn Val Ser Glu Arg
    210             215                 220

Phe Leu Ser Arg Thr Ser Gly Val Tyr Asp Lys Gln Asn Ser Ala Asn
225             230                 235                 240

Phe Ala Pro Asp Thr Ala Ile Asn Ser Asp Ile Ala Gly Gln Gln Tyr
            245             250                 255

Ala Thr Ile Asn Leu His Lys His Phe Asn Asp Leu Gln Ser Pro Ala
            260             265                 270
```

```
Gln Pro Gln Gln Ser Ser Gln Gln Gln Ile Gln Gln Pro Gln His Gln
        275             280             285

Pro Gln His Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
    290             295             300

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
305                 310                 315                 320

Gln Gln Gln His Gln Gln Gln Gln Gln Thr Pro Tyr Pro Ile Val Asn
            325             330             335

Pro Gln Met Val Pro His Ile Pro Ser Glu Asn Ser His Ser Thr Gly
            340             345             350

Leu Met Pro Ser Val Pro Pro Thr Asn Gln Gln Phe Asn Ala Gln Thr
            355             360             365

Gln Ser Ser Met Phe Ser Asp Gln Gln Arg Phe Phe Gln Tyr Gln Leu
    370             375             380

His His Gln Asn Gln Gly Gln Ala Pro Ser Phe Gln Gln Ser Gln Ser
385             390             395             400

Gly Arg Phe Asp Asp Met Asn Ala Met Lys Met Phe Phe Gln Gln Gln
            405             410             415

Ala Leu Gln Gln Asn Ser Leu Gln Gln Asn Leu Gly Asn Gln Asn Tyr
            420             425             430

Gln Ser Asn Thr Arg Asn Asn Thr Ala Glu Glu Thr Thr Pro Thr Asn
    435             440             445

Asp Asn Asn Ala Asn Gly Asn Ser Leu Leu Gln Glu His Ile Arg Ala
    450             455             460

Arg Phe Asn Lys Met Lys Thr Ile Pro Gln Gln Met Lys Asn Gln Ser
465             470             475             480

Thr Val Ala Asn Pro Val Val Ser Asp Ile Thr Ser Gln Gln Gln Tyr
            485             490             495

Met His Met Met Met Gln Arg Met Ala Ala Asn Gln Gln Leu Gln Asn
        500             505             510

Ser Ala Phe Pro Pro Asp Thr Asn Arg Ile Ala Pro Ala Asn Asn Thr
        515             520             525

Met Pro Leu Gln Pro Gly Asn Met Gly Ser Pro Val Ile Glu Asn Pro
        530             535             540

Gly Met Arg Gln Thr Asn Pro Ser Gly Gln Asn Pro Met Ile Asn Met
545             550             555             560

Gln Pro Leu Tyr Gln Asn Val Ser Ser Ala Met His Ala Phe Ala Pro
            565             570             575

Gln Gln Gln Phe His Leu Pro Gln His Tyr Lys Thr Asn Thr Ser Val
            580             585             590

Pro Gln Asn Asp Ser Thr Ser Val Phe Pro Leu Pro Asn Asn Asn Asn
    595             600             605
```

- 36 -

```
Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
    610             615             620
```

```
Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
625             630             635             640
```

```
Thr Pro Thr Val Ser Gln Pro Ser Ser Lys Cys Thr Ser Ser Ser Ser
            645             650             655
```

```
Thr Thr Pro Asn Ile Thr Thr Thr Ile Gln Pro Lys Arg Lys Gln Arg
            660             665             670
```

```
Val Gly Lys Thr Lys Thr Lys Glu Ser Arg Lys Val Ala Ala Ala Gln
        675             680             685
```

```
Lys Val Met Lys Ser Lys Lys Leu Glu Gln Asn Gly Asp Ser Ala Ala
    690             695             700
```

```
Thr Asn Phe Ile Asn Val Thr Pro Lys Asp Ser Gly Gly Lys Gly Thr
705             710             715             720
```

```
Val Lys Val Gln Asn Ser Asn Ser Gln Gln Gln Leu Asn Gly Ser Phe
            725             730             735
```

```
Ser Met Asp Thr Glu Thr Phe Asp Ile Phe Asn Ile Gly Asp Phe Ser
            740             745             750
```

```
Pro Asp Leu Met Asp Ser
            755
```

```
<210> 32
<211> 750
<212> PRT
<213> Saccharomyces cerevisiae
```

```
<400> 32
Met Thr Ser Val Asn Arg Ser Asn Asn Thr Arg Ser Met Ser Ala Ser
  1               5              10              15
```

```
Arg Ser Ala Thr Ser Arg Val Arg Asn Thr Thr Ala Asn Ser Ser Asp
            20              25              30
```

```
Val Asn Ser Ser Lys Arg Asn Ser Asn Ser Val Tyr Asp Asp Asn Ser
            35              40              45
```

```
Ser Lys Arg Arg Ser Arg Arg Ser Asp Gly Lys Asn Asn Asp His Thr
    50              55              60
```

```
Tyr Arg Thr Thr Val Lys Ser Lys Asn Ser Arg Tyr Val Ser Ser Ser
65              70              75              80
```

```
Lys Arg Ala Lys Arg Asn Ser Val Gly Thr Ser Ser Ala Ser Lys Ser
            85              90              95
```

```
Ser Asn Gly Gly Ser Ala His Lys Trp Ser Asn Met Lys Asn Val Ser
            100             105             110
```

```
Asn Ser Ala Val Asp Ala Gly Ser Asp Ser Lys Ser Val Gly Gly Arg
    115             120             125
```

```
Lys Ser Asn Asn Ser Asn Asp Lys Asp Asn Ser Ala Arg Asp Asp Asn
    130             135             140
```

```
Asn Ser Gly Asn Asn Asn Asn Asn Asn Asn His Ser Ser Asn Asn Asn
145                 150                 155                 160

Asp Asn Asn Asn Asn Asn Asn Asp Asp Asn Asn Asn Asn Asn Asn Ser
                165                 170                 175

Asn Ser Arg Asp Asn Asn Asn Asn Ser Asp Asp Ser Asn Arg Asn Asp
            180                 185                 190

Ser Cys Lys Ala Ser Asn Lys Arg Ser Gly Ala Lys Tyr Lys Val Val
        195                 200                 205

Lys Arg Cys Ser Thr Asn Ser Thr Thr Lys Ser Trp Thr Tyr Lys Asn
    210                 215                 220

Thr Asp Val Asn Asn Tyr Val Thr Thr Thr Ala Ser His Asp Val Gly
225                 230                 235                 240

Val Tyr Arg Arg Arg Trp Val Tyr Gly Thr Thr Asp Val Lys Asn Ser
            245                 250                 255

Asn Met Asp Val Cys Cys Thr His Val Val Ser Ser Thr Met Ser Asp
        260                 265                 270

Ser Lys Tyr Ser Thr Trp Arg Gly Asp Ser Arg Met Ala Ala Tyr Ser
        275                 280                 285

Ser Asp Trp Lys Ser Ala His Trp Tyr Thr Ala Met Lys Tyr Tyr Asn
    290                 295                 300

His Gly Lys Tyr Tyr His Met Ser Thr Val Asn Thr Ala Val Asn Gly
305                 310                 315                 320

Lys Ser Val Cys Thr Thr Ser Tyr Met Val Asp Asn Tyr Arg Ala Val
            325                 330                 335

Arg Asn Asn Gly Asn Arg Asn Ser Tyr Lys His Ser Ala Met Ser Ser
            340                 345                 350

Asp Asn Val Val Ser Tyr Lys Gly Asp Ala Asn Gly Cys Asn Asn Ala
    355                 360                 365

Asp Met Val Asn Asp Lys Tyr Arg His Gly Ser Ala Ser His Val Gly
    370                 375                 380

Gly Lys Asn Ala Lys Tyr Lys Arg Lys Asp Lys Lys Arg Lys Lys Ser
385                 390                 395                 400

Ser Asn Asn Asp Ser Ser Val Thr Ser Ser Thr Gly Asn Ser Arg Asn
            405                 410                 415

Asp Asn Asp Asp Asp Met Ser Ser Thr Thr Ser Ser Asp His Asp Ala
            420                 425                 430

Asn Asp Asp Thr Arg Arg Ser Met Thr Asn Ala Trp Thr Lys Asn Met
        435                 440                 445

Thr Ser Lys Cys Gly Val Arg Lys His Gly Gly Ala His Trp Tyr Ser
    450                 455                 460

Cys Lys Ser Ser Ser Asp Val Ser Lys Trp Met Val Lys Arg Ala Trp
465                 470                 475                 480
```

```
Asp Thr Met Val Thr Met Asn Val Val Tyr Asp Asn Thr Ser Asn Ser
                485             490             495

Gly Asp Cys Asp Asp Tyr Asp Lys Ser Ser Asn Gly Gly Cys Trp Gly
            500             505             510

Thr Trp Asp Thr Cys Lys Asn Thr His Ser Ser Ser Asp Asn Gly Lys
    .       515             520             525

Asp Tyr Met Ala Asp Ser Thr Asp Gly Asp Lys Asp Asn Gly Lys Trp
        530             535             540

Lys Arg Ala Cys Arg Thr Arg Ser Arg Ser Gly Val Arg Asn Asp Tyr
545             550             555             560

Arg Ser Ser Asn Thr Asn Gly Ser Val Lys Cys Asn His Asn Asn Val
                565             570             575

Gly Ala Ser Asp Ser Ala Arg Ser Asn Asn Thr Asp His Ala Val Ser
            580             585             590

Val Asn Gly Asp Asn His Tyr Val Gly Tyr Lys Lys Arg Ala Asp Tyr
            595             600             605

Thr Cys Asp Lys Asn Gly Ser Ala Ser Tyr Thr Thr Trp Tyr Val Asn
    610             615             620

Ser Asn Asn Thr Asn Asp Asn Asn Tyr Asn Ser Lys Asn Gly Cys Lys
625             630             635             640

Ser Asp Tyr Asp Lys Thr Thr Tyr Val Asp Ala Thr Ser Trp Arg His
            645             650             655     .

Ser Ala Arg Lys Ala Asn Arg Arg Ala Cys Thr Thr Arg Arg Lys Ser
            660             665             670

Lys Asp Asn Val Met Ala Ala Thr Arg Gly Thr Arg Tyr Tyr Asn Lys
            675             680             685

Val Arg Thr Gly Asn Val Ala Thr His Asn Thr Trp Arg Thr His Val
    690             695             700

Asp Val Ser Val Met Lys Ala Lys Ser Ala Ser Arg Ser Arg Arg Asn
705             710             715             720

Tyr Val Val Ser Asp Asp Asp Ala Met Lys Lys Lys Ala Lys Lys Thr
            725             730             735

Ser Thr Arg·Val Ser Cys Thr Lys Gly Arg His Cys Thr Asp
            740             745             750


<210> 33
<211> 710
<212> PRT
<213> Saccharomyces cerevisiae

<400> 33
Met Asp Asn Lys Arg Tyr Asn Gly Asn Ser Asn Val Asp Gly Thr Tyr
  1           5             10              15

Asp Arg Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val
            20              25              30
```

```
Ser Asp Lys Arg Gly Arg Ser Ser Ser Thr Ser Lys Gly Ser Tyr Arg
        35              40              45
Thr Arg Ala Gly Arg Ser Asp Thr Thr Asn Ser Ser Ala Lys His His
        50              55              60
Ser Lys Lys Ser Thr Val Val Val Val Thr Ser Ser Thr Asp Ser Asn
65              70              75              80
Ser Thr Thr Tyr Ala Arg Val Ser Ser Asp Ser Thr Val Ala Thr Ser
            85              90              95
Ser Thr Thr Thr Arg Thr Arg Thr Arg Asn Asn Thr Val Ser Ser Thr
        100             105             110
Ala Ser Ser Ser Thr Thr Asp Val Gly Asn Ala Thr Ser Ala Asn Trp
        115             120             125
Ser Ala Asn Ala Ser Asn Thr Ser Ser Ser Asp Tyr Ala Thr Ser Tyr
    130             135             140
Thr Arg Lys Ser Thr Asp Asn Tyr Thr Thr Ala Asn Ser Lys Asn Gly
145             150             155             160
Asn Asn Trp Ser Ser Ala Gly Asn Ser Asn Thr Asp His Asn Thr Val
            165             170             175
Asn Arg Arg Ser Ser Ser Thr Thr Asn Arg Val Tyr Thr Asp Ala Tyr
        180             185             190
Tyr Ala Asn Tyr Val Val Arg Val Lys Ser Thr Ser Ser Val Asp Asp
        195             200             205
Val Asp Ala Ser Asn Trp Thr Ala Asn Lys Val Val Asn Ser Ala Thr
    210             215             220
Asn Thr Ser Ser Asn Val Thr His Asn Ala Val Asn Thr Ser Thr Ser
225             230             235             240
Ala Thr Cys Ser Tyr Gly Lys Val Ser Ala Arg Thr Arg Gly Asn Met
            245             250             255
Ala Val Ser Thr Val Ser Ala Cys Ala Ala Gly Lys Ser Lys Val Gly
        260             265             270
Ala Ser Thr Val Ser Ala Arg Val Met Tyr Asn Val Asn Gly Asn Asn
        275             280             285
Thr Lys Asn His Gly Val Asn Tyr Ser Thr Ser Asn Asn Thr Tyr Cys
    290             295             300
Asn Thr Asn Ser His Ser Ser Asn Asn Tyr Ser Ser Asp Ser Lys Lys
305             310             315             320
Asp His Thr Ser Ser Lys Tyr Asp His Asn His Asn Ala Lys Asn Lys
            325             330             335
Gly Val Ser Asp Thr Asn Tyr Gly His Asn Ser Lys Val Lys Arg Lys
        340             345             350
Asp Thr Asp Ala Lys Arg Arg Lys Asp Ser Asn Ser Ser Thr Met Ala
        355             360             365
```

- 40 -

Val Met Asp Ser Ser Asp Tyr Gly Asn Thr Val Lys Asn Ser Ser Asn
    370   375   380

Arg Asp Met Arg Lys Cys Asn Lys Tyr Thr Ser Met Gly Val His Lys
385   390   395   400

Asn Gly Thr Trp Val Cys Lys Lys Met Ala Asn Thr Arg Asn Val Thr
            405   410   415

Ser Gly Val Ser Asp Tyr Cys Thr Asn Asp Gly Asn Tyr Val Gly Lys
            420   425   430

Gly Trp Asn Ser Ser Val Ser His Trp Thr Val Asn Arg Tyr Gly Ser
        435   440   445

Arg Ala Val Arg Ala Cys Ala Asp Ser Thr Cys Thr Thr Ser Val Ser
    450   455   460

Tyr Ala Thr Asp Thr Asn Gly Thr Thr Trp Asp Thr Cys Thr Asn Lys
465   470   475   480

Asn Cys Asp Lys Val Asn Lys Asn Val Lys Cys Cys His Lys Gly Ser
            485   490   495

Thr Val Lys Asn Arg Gly Gly Ala Ser Lys Asn Lys His Ala Asp Gly
        500   505   510

Ser Ser Asp Ser Asp Gly Asn Tyr Gly Thr Tyr Lys Val Thr Ser Arg
        515   520   525

Asp Asn Ser Val Arg Asp Ala Thr Lys Arg Asn Ser Asn Asn Ser Arg
    530   535   540

Val Gly Ser Ser Ala Gly Ser Lys Ser Ser Lys Asn His Arg Lys His
545   550   555   560

Gly His Ser Gly Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser
            565   570   575

Ser Asn Ser Arg His Asn Ser Val Met Asn Asn Ala Gly Thr Ala Asn
        580   585   590

Asn Ala Met Ser Asn Ser Tyr Asn Asn Val Val Tyr Ser Gly Asn Asn
        595   600   605

Asn Asn Gly Asn Ser Asn Gly Asp Asn Ser Asp Ser Arg Ala Asn Gly
    610   615   620

Thr Asn Ser Val Asn Asn Val Ser Asn Asn Asn Asn Tyr Asn Asn
625   630   635   640

Ser Gly Tyr Ser Ser Met Asn Ser Arg Ser Val Ser His Asn Asn Asn
            645   650   655

Asn Asn Thr Asn Asn Tyr Asn Asn Asn Asp Asn Asp Asn Asn Asn Asn
        660   665   670

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
        675   680   685

Asn Ser Asn Asn Ser Asn Asn Asn Asn Asn Asn Asp Thr Ser Tyr Arg
    690   695   700

Tyr Arg Ser Tyr Gly Tyr
705   710

<210> 34
<211> 477
<212> PRT
<213> Saccharomyces cerevisiae

<400> 34
Asp Thr Lys Gly Tyr Asp Asp Asp Ala Ala Thr Asp Gly Lys Lys His
 1   5   10   15

Arg Arg Tyr Arg Tyr Val Ser Gly Ser Val Ser Gly Lys Arg Trp Thr
            20   25   30

Asp Gly Val Ser Trp Ser Ser Arg Ser Gly Lys Tyr Lys Asp Lys Asn
        35   40   45

Ala Gly Ser Asn Ala Asn Ala Thr Ser Ser Gly Ser Thr Asp Ser Ala
    50   55   60

Val Thr Asp Gly Thr Ser Gly Ala Arg Asn Asn Ser Ser Ser Lys Lys
65   70   75   80

Lys Asn His Asp Thr Met Gly His Ser Ser Ser Asp Thr Ser Ser Ser
                85   90   95

Asn Arg Ser Asn Lys Tyr Thr Gly Val Lys Lys Thr Ser Val Lys Lys
            100   105   110

Arg Asn Ser Asn His Val Ser Tyr Tyr Ser Val Lys Asp Lys Asn Cys
            115   120   125

Val Thr Lys Ala Ser Lys Asp Val Arg Ser Val Ala Met Gly Asn Thr
    130   135   140

Thr Gly Asn Val Lys Asn Asn Ser Thr Thr Thr Gly Asn Gly Asn Asn
145   150   155   160

Asn Asn Lys Ser Asn Ser Ser Thr Asn Thr Val Ser Thr Asn Asn Asn
            165   170   175

Ser Ala Asn Asn Ala Ala Gly Ser Asn Thr Ser Ala Asn Lys Asn Tyr
            180   185   190

Tyr Tyr Lys Asn Asp Ser Ser Gly Tyr Thr Ala Ala Ser Thr Thr Met
        195   200   205

Tyr Thr Ala Asn Tyr Thr Ser Asp Asn Thr Asn Ala Thr Gly Met Asn
    210   215   220

Thr His Val Asn Asn Asn Asn Asn Asn Ser Asn Asn Ser Ser Asn Ser
225   230   235   240

Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
            245   250   255

Asn Asn Asn Asn Asn Asn Asn Asn Val Asn Thr Asn Ala Gly Asn Gly
            260   265   270

Asn Asn Asn Arg His Asn Ala Ser Ala Tyr Asn Thr Thr Gly Asp Asn
        275   280   285

- 42 -

```
Gly Ser Tyr Tyr Tyr Thr Thr Asn Asn Asn Tyr Tyr Thr Thr Asn Val
    290             295             300
```

```
Thr Asn Ala Ser Thr Asn Asn Gly Tyr Ser Thr Ser Ser Thr His Tyr
305             310             315                 320
```

```
Tyr Gly His Thr Ser Ser Ala Ser Ala Ala Ala Gly Ala Thr Gly Thr
            325             330                 335
```

```
Gly Thr Ala Asn Val Val Ser Ser Met His Ala Asn Asn Asn Ser Ala
        340             345             350
```

```
Ser Ser Ala Thr Ser Thr Ala Tyr Val Tyr Ser Met Asn Val Asn Val
        355             360             365
```

```
Tyr Tyr Asn Ser Ser Ala Ser Ala Tyr Lys Arg Ala Asn Thr Thr Ser
    370             375             380
```

```
Asn Thr Asn Ala Ser Gly Ala Thr Ser Thr Asn Ser Gly Thr Met Ser
385             390             395             400
```

```
Asn Ala Tyr Ala Asn Ser Tyr Thr Ser Val Tyr Tyr Gly Tyr Ala Met
            405             410             415
```

```
Ala Ser Ala Asn Ser Met Tyr His His His Thr Val Tyr Ala Thr Asn
        420             425             430
```

```
Met Ser Ser Gly His Thr Ser Thr Gly Ser Asp His His His Tyr Asn
        435             440             445
```

```
Asp His Lys Asn Ala Met Gly His Ala Asn Asn Asn Asn Thr Asn Asn
    450             455             460
```

```
Asp Thr Met Asn Asn Asn Thr Asn Thr Ser Thr Thr Thr
465             470             475
```


<210> 35
<211> 454
<212> PRT
<213> Saccharomyces cerevisiae

<400> 35
```
Met Asp Val Arg Ala Ala Cys Ser Ala Ser Gly Arg Thr Gly Lys Lys
  1           5               10                  15
```

```
Gly Tyr Ser Tyr Lys Met Ser Asn Ser Gly Gly Ser Ser Ser Gly Gly
            20              25                  30
```

```
Ser Asp Val Gly Ser Thr Asn Gly Ser Asn Arg Ala Lys Asn Thr Asn
            35              40                  45
```

```
Tyr Lys Lys Thr Asn Lys Lys Tyr Lys Ala Thr Asp Lys Ala Asn Asp
    50              55                  60
```

```
Thr Lys Tyr Tyr Ser Asn Asp Lys Lys Ser Lys Arg Ser Ala Asn Ser
 65              70                  75                      80
```

```
Met Asn Asp Lys Asp Lys Cys Arg Thr Thr Asn Lys Asp Met Thr Arg
                85              90                  95
```

```
Tyr Asp Ser Lys Ser Lys Val Thr Asn Cys Asp His Lys Ala Ser Ser
            100             105                 110
```

His Ser Met Lys Tyr Lys Lys Arg Ser Val Asp Lys Asp His Val Met
     115   120   125

Lys Asp Asp Ser Ser Val Lys Ala Ser Lys Met Asn Ser His Asn Tyr
     130   135   140

Ser Thr Asn Thr Met Asn Lys Met Asp Val Tyr Thr Lys Ala Asn Met
145   150   155   160

Ala Asn Lys Lys Lys Ser Asp Thr Ser Thr Trp Lys Asn Lys Asn Lys
              165   170   175

Ser His Val Ser Tyr Asn Asn Asp Lys Ser Lys Thr Lys Trp Tyr Asn
            180   185   190

Asp Ser Asp Asp Asp Asp Asp Asn Asn Val Asn Asn Asn Asp Asn Asn
            195   200   205

Asn Asn Asn Lys Asn Asp Asn Asn Asn Asp Asn Asn Asn Asp Thr Ser
     210   215   220

Asn Asn Asn Asn Asn Asn Asn Asn Arg Thr Lys Asn Asn Arg Asn Asn
225   230   235   240

Arg Asp Trp Lys Thr Lys Lys Cys Thr Asp Met Asn Asp Lys Arg Asp
            245   250   255

Asn Asn Asn Lys Asn Asp Met Ala Arg Asn Asp Asn Lys Asn Tyr Asn
            260   265   270

Asn Val Asn Lys Arg Asn His Lys Ser Ser Cys Arg Arg Asp Gly Tyr
            275   280   285

Ser Ala Asn Asn Ala Val Asn Ser Thr His Ala Ser Asn Lys Asn Val
          290   295   300

Asn Asp Met Asn Asn Asp Thr Tyr Lys Asn Lys Thr Asp Thr Asn Lys
305   310   315   320

Lys Asn Asp Ser Asn Ser Asn Asp Val Thr Arg Lys Lys Arg Lys Thr
            325   330   335

Ser Asp Gly Asn Tyr Ser Arg Asn Asn Val Ser Val Ser Arg Ser Lys
          340   345   350

Ala Thr Thr Lys Lys Thr Lys Lys Lys Lys Arg Arg Asp Gly Lys Asp
          355   360   365

Lys Lys Asn Lys Lys Asn Ala Asp Asn Lys Lys Asn Asn Ala Val Thr
          370   375   380

Val Ser Val Tyr Asp Ser Asn Lys Val Lys Ser Asn Lys Arg Ser Arg
385   390   395   400

Lys Val Asn Asn Lys Ser Asp Val Val Asn Ser Gly Lys Asp Ser Arg
            405   410   415

Val Lys Ser Cys Lys Lys Tyr Ala Asp Asn Asn Thr Lys Ser Asn Asp
          420   425   430

Ala Asp Gly Trp Asp Asp Met Asn Trp Val Asp Arg Gly Cys Ala Thr
          435   440   445

```
Thr Arg Trp Arg Ala Lys
    450


<210> 36
<211> 284
<212> PRT
<213> Saccharomyces cerevisiae

<400> 36
Met Asn Val Thr Ser Lys Asp Gly Asn His Ser Ser Lys Lys Asn Arg
  1               5                  10                  15

Asn Thr Asn Lys Arg His Lys Asn Ala Ser Asn Asp Arg Asp Ser Val
             20              25                  30

Ser Ser Asn Thr Thr Ser Met Thr Asp Asp Ala Asp Tyr Asn Gly Ala
         35              40                  45

Ser Arg Thr Lys Asn Asn Ser Asp Ser Asp Arg Ser Asn Asp Thr Lys
     50              55                  60

Asn Asn Tyr Asn Lys Arg Thr Gly Tyr Asn Tyr Asn Gly Ser Gly Asn
 65              70              75                      80

Arg Tyr Thr Arg Lys Arg Thr Ala Asn Lys Ala Tyr Ser Asp Asp Asn
             85                  90                  95

Val Lys Asp Asp Asn Asn Thr Lys Lys Ala Ser Arg Ser Ser Gly Arg
            100             105             110

Asn Val Asn Thr Arg Asn Lys Ser Lys Ser His Lys Val Lys Asn Asn
            115             120             125

Lys Ser Ser Ser Arg Lys Ser Ser Ala Ala Arg Lys Gly Lys Tyr Asn
    130             135             140

Ser Asn Ser Asp Ser Thr Thr Arg Lys Val Thr Asp Val Lys Lys Arg
145             150             155             160

Ser Lys Trp His Arg His Asp Lys Lys Met Val Lys Lys Ser Arg Tyr
            165             170             175

Arg Lys Arg Met Arg Gly Thr Asp Val Ser Ser Ser Asp Asn Ser Lys
            180             185             190

Ser Thr Thr Lys Ser Tyr Val Ser Lys Asn Ser Ala Met Asn Asn Asn
            195             200             205

Asp Val Thr Asp Asn Lys Lys Thr Asn Asn Asn Lys Ala Arg Asp Ser
    210             215             220

Met His Thr Lys Lys Asp Thr Lys Asp Asp Thr Asp Ser Lys Lys Arg
225             230             235             240

Lys Val Val Thr Asn Asp Asn Ala Ala Met Val Asn Lys Gly Trp Arg
            245             250             255

Lys Asn Val Met Met Tyr Lys Lys Ser Gly Asn Met Lys Lys Tyr Arg
            260             265             270

Tyr Trp Thr Cys Tyr Cys Asn Tyr Val Tyr Tyr Arg
            275             280
```

- 45 -

<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 37
gggaattccc attaccgaca tttgggcgc   29

<210> 38
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 38
ggggattctg attgattgat tgattgtac   29

<210> 39
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: superbright
      GFP encoding sequence

<220>
<221> CDS
<222> (1)..(720)

<400> 39
atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt   48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
  1   5   10   15

gtt gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga   96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
             20   25   30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att   144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
         35   40   45

tgc act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act   192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
     50   55   60

ttc act tat ggt gtt cag tgc ttt tca aga tac ccg gat cat atg aaa   240
Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65   70   75   80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa   288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                 85   90   95

- 46 -

```
aga act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa    336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100             105             110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt    384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
            115             120             125

att gat ttt aaa gaa gat gga aac att ctt ggg cac aaa ttg gaa tac    432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
            130             135             140

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat    480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145             150             155             160

gga atc aaa gct aac ttc aaa att aga cac aac att gaa gat gga agc    528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
            165             170             175

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc    576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            180             185             190

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt    624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
            195             200             205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt    672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
            210             215             220

gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa tga    720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225             230             235             240


<210> 40
<211> 239
<212> PRT
<213> Artificial Sequence

<400> 40
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
  1             5              10             15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20             25             30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
            35             40             45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
      50             55             60

Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65             70             75             80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                  85             90             95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100             105             110
```

```
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
        130                 135                 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145                     150                 155                 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            180                 185                 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210                 215                 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                     230                 235
```

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<210> 41
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
gaccgcggat ggctagcaaa ggagaag                                      27


<210> 42
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 42
cctgagctct catttgtata gttcatcc                                     28


<210> 43
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
ggaggatcca tggatacgga taagttaatc tcag                              34


<210> 44
<211> 36
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
ggaccgcggg tagcggttct gttgagaaaa gttgcc   36

<210> 45
<211> 7239
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: vector
      containing chimeric gene

<400> 45
gacgaaaggg cctcgtgata cgcctatttt tataggttaa tgtcatgata ataatggttt 60

cttaggacgg atcgcttgcc tgtaacttac acgcgcctcg tatcttttaa tgatggaata 120

atttgggaat ttactctgtg tttatttatt tttatgtttt gtatttggat tttagaaagt 180

aaataaagaa ggtagaagag ttacggaatg aagaaaaaaa ataaacaaa ggtttaaaaa 240

atttcaacaa aaagcgtact ttacatatat atttattaga caagaaaagc agattaaata 300

gatatacatt cgattaacga taagtaaaat gtaaaatcac aggattttcg tgtgtggtct 360

tctacacaga caagatgaaa caattcggca ttaatacctg agagcaggaa gagcaagata 420

aaaggtagta tttgttggcg atccccctag agtcttttac atcttcggaa aacaaaaact 480

attttttctt taatttcttt ttttactttc tattttttaat ttatatattt atattaaaaa 540

atttaaatta taattatttt tatagcacgt gatgaaaagg acccaggtgg cactttttcgg 600

ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg 660

ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt 720

attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt 780

gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg 840

ggttacatcg aactggatct caacagcggt aagatccttg agagttttcg ccccgaagaa 900

cgttttccaa tgatgagcac ttttaaagtt ctgctatgtg gcgcggtatt atcccgtatt 960

gacgccgggc aagagcaact cggtcgccgc atacactatt ctcagaatga cttggttgag 1020

tactcaccag tcacagaaaa gcatcttacg gatggcatga cagtaagaga attatgcagt 1080

gctgccataa ccatgagtga taacactgcg gccaacttac ttctgacaac gatcggagga 1140

ccgaaggagc taaccgcttt tttgcacaac atgggggatc atgtaactcg ccttgatcgt 1200

tgggaaccgg agctgaatga agccatacca aacgacgagc gtgacaccac gatgcctgta 1260

gcaatggcaa caacgttgcg caaactatta actggcgaac tacttactct agcttcccgg 1320

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caacaattaa tagactggat ggaggcggat aaagttgcag gaccacttct gcgctcggcc 1380

cttccggctg gctggtttat tgctgataaa tctggagccg gtgagcgtgg gtctcgcggt 1440

atcattgcag cactggggcc agatggtaag ccctcccgta tcgtagttat ctacacgacg 1500

gggagtcagg caactatgga tgaacgaaat agacagatcg ctgagatagg tgcctcactg 1560

attaagcatt ggtaactgtc agaccaagtt tactcatata tactttagat tgatttaaaa 1620

cttcattttt aatttaaaag gatctaggtg aagatccttt ttgataatct catgaccaaa 1680

atcccttaac gtgagttttc gttccactga gcgtcagacc ccgtagaaaa gatcaaagga 1740

tcttcttgag atcctttttt tctgcgcgta atctgctgct tgcaaacaaa aaaaccaccg 1800

ctaccagcgg tggtttgttt gccggatcaa gagctaccaa ctcttttcc gaaggtaact 1860

ggcttcagca gagcgcagat accaaatact gtccttctag tgtagccgta gttaggccac 1920

cacttcaaga actctgtagc accgcctaca tacctcgctc tgctaatcct gttaccagtg 1980

gctgctgcca gtggcgataa gtcgtgtctt accgggttgg actcaagacg atagttaccg 2040

gataaggcgc agcggtcggg ctgaacgggg ggttcgtgca cacagcccag cttggagcga 2100

acgacctaca ccgaactgag atacctacag cgtgagctat gagaaagcgc cacgcttccc 2160

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agggagcttc caggggggaaa cgcctggtat ctttatagtc ctgtcgggtt cgccacctc 2280

tgacttgagc gtcgattttt gtgatgctcg tcaggggggc ggagcctatg gaaaaacgcc 2340

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gctcgccgca gccgaacgac cgagcgcagc gagtcagtga gcgaggaagc ggaagagcgc 2520

ccaatacgca aaccgcctct ccccgcgcgt tggccgattc attaatgcag ctggcacgac 2580

aggtttcccg actggaaagc gggcagtgag cgcaacgcaa ttaatgtgag ttacctcact 2640

cattaggcac cccaggcttt acactttatg cttccggctc gtatgttgtg tggaattgtg 2700

agcggataac aatttcacac aggaaacagc tatgaccatg attacgccaa gctcggaatt 2760

aaccctcact aaagggaaca aaagctgggt accgggcccc ccctcgaggt cgacggtatc 2820

gataagcttg atatcgaatt cccattaccg acatttgggc gctatacgtg catatgttca 2880

tgtatgtatc tgtatttaaa acacttttgt attatttttc ctcatatatg tgtataggtt 2940

tatacggatg atttaattat tacttcacca cccttttattt caggctgata tcttagcctt 3000

gttactagtt agaaaaagac atttttgctg tcagtcactg tcaagagatt cttttgctgg 3060

catttcttct agaagcaaaa agagcgatgc gtcttttccg ctgaaccgtt ccagcaaaaa 3120

agactaccaa cgcaatatgg attgtcagaa tcatataaaa gagaagcaaa taactccttg 3180

tcttgtatca attgcattat aatatcttct tgttagtgca atatcatata gaagtcatcg 3240
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- 50 -

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aaatagatat taagaaaaac aaactgtaca atcaatcaat caatcaggat ccatggatac 3300

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tgcgaagttg acatccgcag ctcagtcgaa ccccaatgac gagcaaatgt caactattga 3420

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ctcgcaagat cgtgctgctg gtggtggttc atcttttatg aacactttaa tggcagactc 3540

taagggttct tcccaaacgc aactaggaaa actagctttg ttagccacag tgatgacaca 3600

ctcatcaaat aaaggttctt ctaacagagg gtttgacgta gggactgtca tgtcaatgct 3660

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tcaattcttt aagtcaggta acaattccca aggtcaggga caaggtcaag gtcaaggtca 3780

aggtcaagga caaggtcaag gtcaaggttc ttttactgct ttggcgtctt tggcttcatc 3840

tttcatgaat tccaacaaca ataatcagca aggtcaaaat caaagctccg gtggttcctc 3900

ctttggagca ctagcttcta tggcaagttc ttttatgcat tccaataata atcagaactc 3960

caacaatagt caacagggtt ataaccaatc ctatcaaaac ggtaaccaaa atagtcaagg 4020

ttacaataat caacagtacc aaggtggcaa cggtggttac caacaacaac agggacaatc 4080

tggtggtgct ttttcctcat tggcctccat ggctcaatct tacttaggtg gtggacaaac 4140

tcaatccaac caacagcaat acaatcaaca aggccaaaac aaccagcagc aataccagca 4200

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acaacaatct aatgagtacg gaagaccgca atacggcgga aaccagaact ccaatggaca 4440

gcacgaatcc tttaattttt ctggcaactt ttctcaacag aacaataacg gcaaccagaa 4500

ccgctacccg cggatggcta gcaaaggaga agaactcttc actggagttg tcccaattct 4560

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cattcttggg cacaaattgg aatacaacta taactcacac aatgtataca tcatggcaga 4980

caaacaaaag aatggaatca aagctaactt caaaattaga cacaacattg aagatggaag 5040

cgttcaacta gcagaccatt atcaacaaaa tactccaatt ggcgatggcc ctgtcctttt 5100

accagacaac cattacctgt ccacacaatc tgccctttcg aaagatccca acgaaaagag 5160
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- 51 -

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agaccacatg gtccttcttg agtttgtaac agctgctggg attacacatg gcatggatga 5220

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aaccttcatc tcttccaccc atgtctcttt gagcaataaa gccgataaca aaatctttgt 6300

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cactacatat gcgtatatat accaatctaa gtctgtgctc cttccttcgt tcttccttct 6960

gttcggagat taccgaatca aaaaaatttc aaagaaaccg aaatcaaaaa aagaataaa 7020

aaaaaaatga tgaattgaat tgaaaagctg tggtatggtg cactctcagt acaatctgct 7080
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ctgatgccgc atagttaagc cagccccgac acccgccaac acccgctgac gcgccctgac 7140

gggcttgtct gctcccggca tccgcttaca gacaagctgt gaccgtctcc gggagctgca 7200

tgtgtcagag gttttcaccg tcatcaccga aacgcgcga                         7239
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<210> 46
<211> 741
<212> PRT
<213> Pichia pinus

<400> 46

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Met Ser Gln Asp Gln Gln Gln Gln Gln Phe Asn Ala Asn Asn Leu
 1               5                  10                  15

Ala Gly Asn Val Gln Asn Ile Asn Leu Asn Ala Pro Ala Tyr Asp Pro
            20                  25                  30

Ala Val Gln Ser Tyr Ile Pro Asn Thr Ala Gln Ala Phe Val Pro Ser
        35                  40                  45

Ala Gln Pro Tyr Ile Pro Gly Gln Gln Glu Gln Gln Phe Gly Gln Tyr
     50                  55                  60

Gly Gln Gln Gln Gln Asn Tyr Asn Gln Gly Gly Tyr Asn Asn Tyr Asn
 65                  70                  75                  80

Asn Arg Gly Gly Tyr Ser Asn Asn Arg Gly Gly Tyr Asn Asn Ser Asn
                85                  90                  95

Arg Gly Gly Tyr Ser Asn Tyr Asn Ser Tyr Asn Thr Asn Ser Asn Gln
            100                 105                 110

Gly Gly Tyr Ser Asn Tyr Asn Asn Asn Tyr Ala Asn Asn Ser Tyr Asn
            115                 120                 125

Asn Asn Asn Asn Tyr Asn Asn Asn Tyr Asn Gln Gly Tyr Asn Asn Tyr
        130                 135                 140

Asn Ser Gln Pro Gln Gly Gln Asp Gln Gln Gln Glu Thr Gly Ser Gly
145                 150                 155                 160

Gln Met Ser Leu Glu Asp Tyr Gln Lys Gln Gln Lys Glu Ser Leu Asn
                165                 170                 175

Lys Leu Asn Thr Lys Pro Lys Lys Val Leu Lys Leu Asn Leu Asn Ser
            180                 185                 190

Ser Thr Val Lys Ala Pro Ile Val Thr Lys Lys Lys Glu Glu Glu Pro
            195                 200                 205

Val Asn Gln Glu Ser Lys Thr Glu Glu Pro Ala Lys Glu Glu Ile Lys
     210                 215                 220

Asn Gln Glu Pro Ala Glu Ala Glu Asn Lys Val Glu Glu Glu Ser Lys
225                 230                 235                 240

Val Glu Ala Pro Thr Ala Ala Lys Pro Val Ser Glu Ser Glu Phe Pro
                245                 250                 255

Ala Ser Thr Pro Lys Thr Glu Ala Lys Ala Ser Lys Glu Val Ala Ala
                260                 265                 270
```

```
Ala Ala Ala Ala Leu Lys Lys Glu Val Ser Gln Ala Lys Lys Glu Ser
        275             280             285

Asn Val Thr Asn Ala Asp Ala Leu Val Lys Glu Gln Glu Glu Gln Ile
        290             295             300

Asp Ala Ser Ile Val Asn Asp Met Phe Gly Gly Lys Asp His Met Ser
305             310             315             320

Ile Ile Phe Met Gly His Val Asp Ala Gly Lys Ser Thr Met Gly Gly
            325             330             335

Asn Leu Leu Phe Leu Thr Gly Ala Val Asp Lys Arg Thr Val Glu Lys
        340             345             350

Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg Gln Gly Trp Tyr Leu Ser
        355             360             365

Trp Ile Met Asp Thr Asn Lys Glu Glu Arg Asn Asp Gly Lys Thr Ile
    370             375             380

Glu Val Gly Lys Ser Tyr Phe Glu Thr Asp Lys Arg Arg Tyr Thr Ile
385             390             395             400

Leu Asp Ala Pro Gly His Lys Leu Tyr Ile Ser Glu Met Ile Gly Gly
            405             410             415

Ala Ser Gln Ala Asp Val Gly Val Leu Val Ile Ser Ser Arg Lys Gly
        420             425             430

Glu Tyr Glu Ala Gly Phe Glu Arg Gly Gly Gln Ser Arg Glu His Ala
        435             440             445

Ile Leu Ala Lys Thr Gln Gly Val Asn Lys Leu Val Val Val Ile Asn
    450             455             460

Lys Met Asp Asp Pro Thr Val Asn Trp Ser Lys Glu Arg Tyr Glu Glu
465             470             475             480

Cys Thr Thr Lys Leu Ala Met Tyr Leu Lys Gly Val Gly Tyr Gln Lys
            485             490             495

Gly Asp Val Leu Phe Met Pro Val Ser Gly Tyr Thr Gly Ala Gly Leu
        500             505             510

Lys Glu Arg Val Ser Gln Lys Asp Ala Pro Trp Tyr Asn Gly Pro Ser
        515             520             525

Leu Leu Glu Tyr Leu Asp Ser Met Pro Leu Ala Val Arg Lys Ile Asn
        530             535             540

Asp Pro Phe Met Leu Pro Ile Ser Ser Lys Met Lys Asp Leu Gly Thr
545             550             555             560

Val Ile Glu Gly Lys Ile Glu Ser Gly His Val Lys Lys Gly Gln Asn
            565             570             575

Leu Leu Val Met Pro Asn Lys Thr Gln Val Glu Val Thr Thr Ile Tyr
        580             585             590

Asn Glu Thr Glu Ala Glu Ala Asp Ser Ala Phe Cys Gly Glu Gln Val
        595             600             605
```

- 54 -

Arg Leu Arg Leu Arg Gly Ile Glu Glu Glu Asp Leu Ser Ala Gly Tyr
    610   615   620

Val Leu Ser Ser Ile Asn His Pro Val Lys Thr Val Thr Arg Phe Glu
625   630   635   640

Ala Gln Ile Ala Ile Val Glu Leu Lys Ser Ile Leu Ser Thr Gly Phe
            645   650   655

Ser Cys Val Met His Val His Thr Ala Ile Glu Glu Val Thr Phe Thr
            660   665   670

Gln Leu Leu His Asn Leu Gln Lys Gly Thr Asn Arg Arg Ser Lys Lys
            675   680   685

Ala Pro Ala Phe Ala Lys Gln Gly Met Lys Ile Ile Ala Val Leu Glu
    690   695   700

Thr Thr Glu Pro Val Cys Ile Glu Ser Tyr Asp Asp Tyr Pro Gln Leu
705   710   715   720

Gly Arg Phe Thr Leu Arg Asp Gln Gly Gln Thr Ile Ala Ile Gly Lys
            725   730   735

Val Thr Lys Leu Leu
        740

<210> 47
<211> 715
<212> PRT
<213> Candida albicans

<400> 47
Met Ala Asn Ala Ser Leu Asn Gly Asp Gln Ser Lys Gln Gln Gln Gln
  1   5   10   15

Gln Gln Gln Gln Gln Gln Gln Gln Gln Asn Tyr Tyr Asn Pro Asn Ala
            20   25   30

Ala Gln Ser Phe Val Pro Gln Gly Gly Tyr Gln Gln Phe Gln Gln Phe
            35   40   45

Gln Pro Gln Gln Gln Gln Gln Gln Tyr Gly Gly Tyr Asn Gln Tyr Asn
    50   55   60

Gln Tyr Gln Gly Gly Tyr Gln Gln Asn Tyr Asn Asn Arg Gly Gly Tyr
65   70   75   80

Gln Gln Gly Tyr Asn Asn Arg Gly Gly Tyr Gln Gln Asn Tyr Asn Asn
            85   90   95

Arg Gly Gly Tyr Gln Gly Tyr Asn Gln Asn Gln Gln Tyr Gly Gly Tyr
            100   105   110

Gln Gln Tyr Asn Ser Gln Pro Gln Gln Gln Gln Gln Gln Ser Gln
            115   120   125

Gly Met Ser Leu Ala Asp Phe Gln Lys Gln Lys Thr Glu Gln Gln Ala
    130   135   140

Ser Leu Asn Lys Pro Ala Val Lys Lys Thr Leu Lys Leu Ala Gly Ser
145   150   155   160

- 55 -

```
Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Asp Thr Thr Ser
            165             170         175

Lys Pro Gln Ser Lys Glu Ser Ser Pro Ala Pro Ala Pro Ala Ala Ser
            180             185         190

Ala Ser Ala Ser Ala Pro Gln Glu Glu Lys Lys Glu Glu Lys Glu Ala
            195             200         205

Ala Ala Ala Thr Pro Ala Ala Ala Pro Glu Thr Lys Lys Glu Thr Ser
    210             215             220

Ala Pro Ala Glu Thr Lys Lys Glu Ala Thr Pro Thr Pro Ala Ala Lys
225             230             235             240

Asn Glu Ser Thr Pro Ile Pro Ala Ala Ala Ala Lys Lys Glu Ser Thr
            245             250             255

Pro Val Ser Asn Ser Ala Ser Val Ala Thr Ala Asp Ala Leu Val Lys
            260             265         270

Glu Gln Glu Asp Glu Ile Asp Glu Glu Val Val Lys Asp Met Phe Gly
            275             280         285

Gly Lys Asp His Val Ser Ile Ile Phe Met Gly His Val Asp Ala Gly
    290             295         300

Lys Ser Thr Met Gly Gly Asn Ile Leu Tyr Leu Thr Gly Ser Val Asp
305             310             315             320

Lys Arg Thr Val Glu Lys Tyr Glu Arg Glu Ala Lys Asp Ala Gly Arg
            325             330         335

Gln Gly Trp Tyr Leu Ser Trp Val Met Asp Thr Asn Lys Glu Glu Arg
            340             345         350

Asn Asp Gly Lys Thr Ile Glu Val Gly Lys Ala Tyr Phe Glu Thr Asp
            355             360         365

Lys Arg Arg Tyr Thr Ile Leu Asp Ala Pro Gly His Lys Met Tyr Val
    370             375         380

Ser Glu Met Ile Gly Gly Ala Ser Gln Ala Asp Val Gly Ile Leu Val
385             390             395             400

Ile Ser Ala Arg Lys Gly Glu Tyr Glu Thr Gly Phe Glu Lys Gly Gly
            405             410         415

Gln Thr Arg Glu His Ala Leu Leu Ala Lys Thr Gln Gly Val Asn Lys
            420             425         430

Ile Ile Val Val Val Asn Lys Met Asp Asp Ser Thr Val Gly Trp Ser
            435             440         445

Lys Glu Arg Tyr Gln Glu Cys Thr Thr Lys Leu Gly Ala Phe Leu Lys
    450             455         460

Gly Ile Gly Tyr Ala Lys Asp Asp Ile Ile Tyr Met Pro Val Ser Gly
465             470             475             480

Tyr Thr Gly Ala Gly Leu Lys Asp Arg Val Asp Pro Lys Asp Cys Pro
            485             490         495
```

Trp Tyr Asp Gly Pro Ser Leu Leu Glu Tyr Leu Asp Asn Met Asp Thr
            500   505   510

Met Asn Arg Lys Ile Asn Gly Pro Phe Met Met Pro Val Ser Gly Lys
            515   520   525

Met Lys Asp Leu Gly Thr Ile Val Glu Gly Lys Ile Glu Ser Gly His
    530   535   540

Val Lys Lys Gly Thr Asn Leu Ile Met Met Pro Asn Lys Thr Pro Ile
545   550   555   560

Glu Val Leu Thr Ile Phe Asn Glu Thr Glu Gln Glu Cys Asp Thr Ala
                565   570   575

Phe Ser Gly Glu Gln Val Arg Leu Lys Ile Lys Gly Ile Glu Glu Glu
            580   585   590

Asp Leu Gln Pro Gly Tyr Val Leu Thr Ser Pro Lys Asn Pro Val Lys
        595   600   605

Thr Val Thr Arg Phe Glu Ala Gln Ile Ala Ile Val Glu Leu Lys Ser
    610   615   620

Ile Leu Ser Asn Gly Phe Ser Cys Val Met His Leu His Thr Ala Ile
625   630   635   640

Glu Glu Val Lys Phe Ile Glu Leu Lys His Lys Leu Glu Lys Gly Thr
                645   650   655

Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe Ala Lys Lys Gly Met Lys
            660   ·   665   670

Ile Ile Ala Ile Leu Glu Val Gly Glu Leu Val Cys Ala Glu Thr Tyr
        675   680   685

Lys Asp Tyr Pro Gln Leu Gly Arg Phe Thr Leu Arg Asp Gln Gly Thr
    690   695   700

Thr Ile Ala Ile Gly Lys Ile Thr Lys Leu Leu
705   710   715

<210> 48
<211> 653
<212> DNA
<213> Saccharomyces cerevisiae

<400> 48
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tgccaaaata gggggcgggt tacacagaat atataacact gatggtgctt gggtgaacag 180

gtttattcct ggcatccact aaatataatg gagcccgctt tttaagctgg catccagaaa 240

aaaaaagaat cccagcacca aaatattgtt ttcttcacca accatcagtt cataggtcca 300

ttctcttagc gcaactacag agaacagggc acaaacaggc aaaaaacggg cacaacctca 360

atggagtgat gcaacctgcc tggagtaaat gatgacacaa ggcaattgac ccacgcatgt 420

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gaaaaaaaag gtttaaacca gttccctgaa attattcccc tacttgacta ataagtatat 540

aaagacggta ggtattgatt gtaattctgt aaatctattt cttaaacttc ttaaattcta 600

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<210> 49
<211> 7988
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ure2N-Sup35C
      integration plasmid

<400> 49
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ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180

accataccac agcttttcaa ttcaattcat catttttttt ttattctttt ttttgatttc 240

ggtttctttg aaattttttt gattcggtaa tctccgaaca gaaggaagaa cgaaggaagg 300

agcacagact tagattggta tatatacgca tatgtagtgt tgaagaaaca tgaaattgcc 360

cagtattctt aacccaactg cacagaacaa aaacctgcag gaaacgaaga taaatcatgt 420

cgaaagctac atataaggaa cgtgctgcta ctcatcctag tcctgttgct gccaagctat 480

ttaatatcat gcacgaaaag caaacaaact tgtgtgcttc attggatgtt cgtaccacca 540

aggaattact ggagttagtt gaagcattag gtcccaaaat ttgtttacta aaaacacatg 600

tggatatctt gactgatttt tccatggagg gcacagttaa gccgctaaag gcattatccg 660

ccaagtacaa ttttttactc ttcgaagaca gaaaatttgc tgacattggt aatacagtca 720

aattgcagta ctctgcgggt gtatacagaa tagcagaatg gcagacatt acgaatgcac 780

acggtgtggt gggcccaggt attgttagcg gtttgaagca ggcggcagaa gaagtaacaa 840

aggaacctag aggccttttg atgttagcag aattgtcatg caagggctcc ctatctactg 900

gagaatatac taagggtact gttgacattg cgaagagcga caaagatttt gttatcggct 960

ttattgctca aagagacatg ggtggaagag atgaaggtta cgattggttg attatgacac 1020

ccggtgtggg tttagatgac aagggagacg cattgggtca acagtataga accgtggatg 1080

atgtggtctc tacaggatct gacattatta ttgttggaag aggactattt gcaaagggaa 1140

gggatgctaa ggtagagggt gaacgttaca gaaaagcagg ctggaagca tatttgagaa 1200

gatgcggcca gcaaaactaa aaaactgtat tataagtaaa tgcatgtata ctaaactcac 1260

aaattagagc ttcaatttaa ttatatcagt tattacccta tgcggtgtga ataccgcac 1320
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tcccttataa atcaaaagaa tagaccgaga tagggttgag tgttgttcca gtttggaaca 1500

agagtccact attaaagaac gtggactcca acgtcaaagg gcgaaaaacc gtctatcagg 1560

gcgatggccc actacgtgaa ccatcaccct aatcaagttt tttggggtcg aggtgccgta 1620

aagcactaaa tcggaaccct aaagggagcc cccgatttag agcttgacgg ggaaagccgg 1680

cgaacgtggc gagaaaggaa gggaagaaag cgaaaggagc gggcgctagg gcgctggcaa 1740

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tccatgtcac taatagattt tgcacattct gaaataacgc cggggaaggg ttatgatgaa 2580

aacgtgattg aaggagttga aaccttgcta gatattttta tgaaattcta gatatattga 2640

gaggtgaagt ttaccttgtt tatggtatat ggtacaaaaa gaactaaact aattatacgt 2700

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aatgctttat gatcggtatt attgtgtttg catttactta tgtttgcaag aaatggatcc 2820

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taaaacagcg atgaccttca tacccttctt agcaaaagca ggtggtttct ttgacttacg 3000

gttggtaccc ttttctaatt tgtgcaataa cttaacaata tgtacctctt caattgctgt 3060

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aatttgagct acaaacttgg taacactctt gatagggttc tttggcgatg ttagtacaaa 3180

acctggtgaa atgtcttctt cttcaacacc tttgattctt agtttaactt gctcaccaca 3240
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- 59 -

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catagccata tcaacttcat tttcagtttc gttgtaaata ttttgaattt ccacagcggt 3300

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gatgtgacgg tcgacgtggt tcattgtatc cagatattct aacagagttg ggccggtgta 3480

ccatgggcat tcttttggat ctacgtgatc tttcaaattt gcaccactgt agccggatac 3540

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- 60 -

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gatacgggag ggcttaccat ctggccccag tgctgcaatg·ataccgcgag acccacgctc 7080
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- 61 -

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cgtctaagaa accattatta tcatgacatt aacctataaa aataggcgta tcacgaggcc 7980

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<210> 50
<211> 405
<212> PRT
<213> Saccharomyces cerevisiae

<400> 50

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Met Asp Thr Asp Lys Leu Ile Ser Glu Ala Glu Ser His Phe Ser Gln
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Gly Asn His Ala Glu Ala Val Ala Lys Leu Thr Ser Ala Ala Gln Ser
            20                  25                  30

Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
        35                  40                  45

Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
    50                  55                  60

Gln Asp Arg Ala Ala Gly Gly Gly Ser Ser Phe Met Asn Thr Leu Met
 65                  70                  75                  80

Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
                85                  90                  95

Leu Ala Thr Val Met Thr His Ser Ser Asn Lys Gly Ser Ser Asn Arg
            100                 105                 110

Gly Phe Asp Val Gly Thr Val Met Ser Met Leu Ser Gly Ser Gly Gly
            115                 120                 125
```

- 62 -

```
Gly Ser Gln Ser Met Gly Ala Ser Gly Leu Ala Ala Leu Ala Ser Gln
    130             135             140

Phe Phe Lys Ser Gly Asn Asn Ser Gln Gly Gln Gly Gln Gly Gln Gly
145             150             155             160

Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Ser Phe Thr Ala
            165             170             175

Leu Ala Ser Leu Ala Ser Ser Phe Met Asn Ser Asn Asn Asn Asn Gln
        180             185             190

Gln Gly Gln Asn Gln Ser Ser Gly Gly Ser Ser Phe Gly Ala Leu Ala
        195             200             205

Ser Met Ala Ser Ser Phe Met His Ser Asn Asn Asn Gln Asn Ser Asn
    210             215             220

Asn Ser Gln Gln Gly Tyr Asn Gln Ser Tyr Gln Asn Gly Asn Gln Asn
225             230             235             240

Ser Gln Gly Tyr Asn Asn Gln Gln Tyr Gln Gly Gly Asn Gly Gly Tyr
            245             250             255

Gln Gln Gln Gln Gly Gln Ser Gly Gly Ala Phe Ser Ser Leu Ala Ser
        260             265             270

Met Ala Gln Ser Tyr Leu Gly Gly Gly Gln Thr Gln Ser Asn Gln Gln
        275             280             285

Gln Tyr Asn Gln Gln Gly Gln Asn Asn Gln Gln Gln Tyr Gln Gln Gln
    290             295             300

Gly Gln Asn Tyr Gln His Gln Gln Gln Gly Gln Gln Gln Gln Gly
305             310             315             320

His Ser Ser Ser Phe Ser Ala Leu Ala Ser Met Ala Ser Ser Tyr Leu
            325             330             335

Gly Asn Asn Ser Asn Ser Asn Ser Ser Tyr Gly Gly Gln Gln Gln Ala
        340             345             350

Asn Glu Tyr Gly Arg Pro Gln His Asn Gly Gln Gln Gln Ser Asn Glu
        355             360             365

Tyr Gly Arg Pro Gln Tyr Gly Gly Asn Gln Asn Ser Asn Gly Gln His
    370             375             380

Glu Ser Phe Asn Phe Ser Gly Asn Phe Ser Gln Gln Asn Asn Asn Gly
385             390             395             400

Asn Gln Asn Arg Tyr
            405


<210> 51
<211> 128
<212> PRT
<213> Saccharomyces cerevisiae

<400> 51
Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Glu Lys Ser Gln
  1             5               10              15
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- 63 -

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Tyr Ser Arg Pro Ser Asn Pro Pro Pro Ser Ser Ala His Gln Asn Lys
            20              25                  30

Thr Gln Glu Arg Gly Tyr Pro Pro Gln Gln Gln Gln Tyr Tyr Gln
        35              40                  45

Gln Gln Gln Gln His Pro Gly Tyr Tyr Asn Gln Gln Gly Tyr Asn Gln
    50              55                  60

Gln Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln
65              70                  75                  80

Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln Gly His Gln Gln Pro Val
            85              90                  95

Tyr Val Gln Gln Gln Pro Pro Gln Arg Gly Asn Glu Gly Cys Leu Ala
        100             105                 110

Ala Cys Leu Ala Ala Leu Cys Ile Cys Cys Thr Met Asp Met Leu Phe
        115             120                 125
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<210> 52
<211> 534
<212> PRT
<213> Saccharomyces cerevisiae

<400> 52
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Met Ser Ser Asp Glu Glu Asp Phe Asn Asp Ile Tyr Gly Asp Asp Lys
 1           5                  10                  15

Pro Thr Thr Thr Glu Glu Val Lys Lys Glu Glu Glu Gln Asn Lys Ala
            20              25                  30

Gly Ser Gly Thr Ser Gln Leu Asp Gln Leu Ala Ala Leu Gln Ala Leu
        35              40                  45

Ser Ser Ser Leu Asn Lys Leu Asn Asn Pro Asn Ser Asn Asn Ser Ser
    50              55                  60

Ser Asn Asn Ser Asn Gln Asp Thr Ser Ser Ser Lys Gln Asp Gly Thr
65              70                  75                  80

Ala Asn Asp Lys Glu Gly Ser Asn Glu Asp Thr Lys Asn Glu Lys Lys
            85              90                  95

Gln Glu Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn Ala Ser Ser Ala
        100             105                 110

Gly Pro Ser Gly Leu Pro Trp Glu Gln Leu Gln Gln Thr Met Ser Gln
        115             120                 125

Phe Gln Gln Pro Ser Ser Gln Ser Pro Pro Gln Gln Gln Val Thr Gln
    130             135                 140

Thr Lys Glu Glu Arg Ser Lys Ala Asp Leu Ser Lys Glu Ser Cys Lys
145             150                 155                 160

Met Phe Ile Gly Gly Leu Asn Trp Asp Thr Thr Glu Asp Asn Leu Arg
            165             170                 175
```

Glu Tyr Phe Gly Lys Tyr Gly Thr Val Thr Asp Leu Lys Ile Met Lys
            180   185   190

Asp Pro Ala Thr Gly Arg Ser Arg Gly Phe Gly Phe Leu Ser Phe Glu
            195   200   205

Lys Pro Ser Ser Val Asp Glu Val Val Lys Thr Gln His Ile Leu Asp
    210   215   220

Gly Lys Val Ile Asp Pro Lys Arg Ala Ile Pro Arg Asp Glu Gln Asp
225   230   235   240

Lys Thr Gly Lys Ile Phe Val Gly Gly Ile Gly Pro Asp Val Arg Pro
            245   250   255

Lys Glu Phe Glu Glu Phe Phe Ser Gln Trp Gly Thr Ile Ile Asp Ala
            260   265   270

Gln Leu Met Leu Asp Lys Asp Thr Gly Gln Ser Arg Gly Phe Gly Phe
            275   280   285

Val Thr Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Gln Asn Lys
    290   295   300

Phe Ile Asp Phe Lys Asp Arg Lys Ile Glu Ile Lys Arg Ala Glu Pro
305   310   315   320

Arg His Met Gln Gln Lys Ser Ser Asn Asn Gly Gly Asn Asn Gly Gly
            325   330   335

Asn Asn Met Asn Arg Arg Gly Gly Asn Phe Gly Asn Gln Gly Asp Phe
            340   345   350

Asn Gln Met Tyr Gln Asn Pro Met Met Gly Gly Tyr Asn Pro Met Met
            355   360   365

Asn Pro Gln Ala Met Thr Asp Tyr Tyr Gln Lys Met Gln Glu Tyr Tyr
    370   375   380

Gln Gln Met Gln Lys Gln Thr Gly Met Asp Tyr Thr Gln Met Tyr Gln
385   390   395   400

Gln Gln Met Gln Gln Met Ala Met Met Met Pro Gly Phe Ala Met Pro
            405   410   415

Pro Asn Ala Met Thr Leu Asn Gln Pro Gln Gln Asp Ser Asn Ala Thr
            420   425   430

Gln Gly Ser Pro Ala Pro Ser Asp Ser Asp Asn Asn Lys Ser Asn Asp
            435   440   445

Val Gln Thr Ile Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Pro Pro
    450   455   460

Leu Asn Leu Pro Asn Gly Pro Lys Gly Pro Ser Gln Tyr Asn Asp Asp
465   470   475   480

His Asn Ser Gly Tyr Gly Tyr Asn Arg Asp Arg Gly Asp Arg Asp Arg
            485   490   495

Asn Asp Arg Asp Arg Asp Tyr Asn His Arg Ser Gly Gly Asn His Arg
            500   505   510

Arg Asn Gly Arg Gly Gly Arg Gly Gly Tyr Asn Arg Arg Asn Asn Gly
        515   520   525

Tyr His Pro Tyr Asn Arg
    530

<210> 53
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 53
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<210> 54
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 54
ccaagctttc agtagcggtt ctgttgagaa aagttg   36

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
ggtgtcttgg ccaattgccc   20

<210> 56
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
gtcgacctgc agcgtacgca tttcagatct ttgctatac   39

<210> 57
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
cgagctcgaa ttcatcgatt gattcagttc gccttctatc   40

<210> 58
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
ctgttttgaa agggtccaca tg   22

<210> 59
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 60
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 61
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 62
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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 62
cggaattcct cgagaagata tccatc   26

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 63
gggatcctgt tgctagtggg caga   24

<210> 64
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 64
gtaccgcgga tgtctttgaa cgactttcaa aagc   34

<210> 65
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 65
gtggagctct tactcggcaa ttttaacaat tttac   35

<210>   66
<211>   3153
<212>   DNA
<213>   Saccharomycees cerevisia

<400>   66
atgtcggatt caaaccaagg caacaatcag caaaactacc agcaatacag ccagaacggt   60

aaccaacaac aaggtaacaa cagataccaa ggttatcaag cttacaatgc tcaagcccaa   120

cctgcaggtg ggtactacca aaattaccaa ggttattctg ggtaccaaca aggtggctat   180

caacagtaca atcccgacgc cggttaccag caacagtata atcctcaagg aggctatcaa   240

cagtacaatc ctcaaggcgg ttatcagcag caattcaatc cacaaggtgg ccgtggaaat   300

tacaaaaact tcaactacaa taacaatttg caaggatatc aagctggttt ccaaccacag   360

tctcaaggta tgtctttgaa cgactttcaa aagcaacaaa gcaggccgc tcccaaacca   420

aagaagactt tgaagcttgt ctccagttcc ggtatcaagt tggccaatgc taccaagaag   480

gttggcacaa aacctgccga atctgataag aaagaggaag agaagtctgc tgaaaccaaa   540

gaaccaacta agagccaac aaaggtcgaa gaaccagtta aaaaggagga gaaaccagtc   600

cagactgaag aaaagacgga ggaaaaatcg gaacttccaa aggtagaaga ccttaaaatc   660

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tctgaatcaa cacataatac caacaatgcc aatgttacca gtgctgatgc cttgatcaag    720

gaacaggaag aagaagtgga tgacgaagtt gttaacgatc cgcggatgga ctccaaagaa    780

tccttagctc cccctggtag agacgaagtc cctggcagtt tgcttggcca agggaggggg    840

agcgtaatgg acttttataa aagcctgagg ggaggagcta cagtcaaggt ttctgcatct    900

tcgccctcag tggctgctgc ttctcaggca gattccaagc agcagaggat tctccttgat    960

ttctcgaaag gctccacaag caatgtgcag cagcgacagc agcagcagca gcagcagcag   1020

cagcagcagc agcagcagca gcagcagcag cagccaggct tatccaaagc cgtttcactg   1080

tccatggggc tgtatatggg agagacagaa acaaaagtga tggggaatga cttgggctac   1140

ccacagcagg gccaacttgg cctttcctct ggggaaacag actttcggct tctggaagaa   1200

agcattgcaa acctcaatag gtcgaccagc gttccagaga accccaagag ttcaacgtct   1260

gcaactgggt gtgctacccc gacagagaag gagtttccca aaactcactc ggatgcatct   1320

tcagaacagc aaaatcgaaa aagccagacc ggcaccaacg gaggcagtgt gaaattgtat   1380

cccacagacc aaagcacctt tgacctcttg aaggatttgg agttttccgc tgggtcccca   1440

agtaaagaca caaacgagag tccctggaga tcagatctgt tgatagatga aaacttgctt   1500

tctcctttgg cgggagaaga tgatccattc cttctcgaag ggaacacgaa tgaggattgt   1560

aagcctctta ttttaccgga cactaaacct aaaattaagg atactggaga tacaatctta   1620

tcaagtccca gcagtgtggc actaccccaa gtgaaaacag aaaaagatga tttcattgaa   1680

ctttgcaccc ccggggtaat taagcaagag aaactgggcc cagtttattg tcaggcaagc   1740

ttttctggga caaatataat tggtaataaa atgtctgcca tttctgttca tggtgtgagt   1800

acctctggag gacagatgta ccactatgac atgaatacag catccctttc tcagcagcag   1860

gatcagaagc ctgtttttaa tgtcattcca ccaattcctg ttggttctga aaactggaat   1920

aggtgccaag gctccggaga ggacagcctg acttccttgg gggctctgaa cttcccaggc   1980

cggtcagtgt tttctaatgg gtactcaagc cctggaatga gaccagatgt aagctctcct   2040

ccatccagct cgtcagcagc cacgggacca cctcccaagc tctgcctggt gtgctccgat   2100

gaagcttcag gatgtcatta cggggtgctg acatgtggaa gctgcaaagt attctttaaa   2160

agagcagtgg aaggacagca caattacctt tgtgctggaa gaaacgattg catcattgat   2220

aaaattcgaa ggaaaaactg cccagcatgc cgctatcgga atgtcttca ggctggaatg   2280

aaccttgaag ctcgaaaaac aaagaaaaaa atcaaaggga ttcagcaagc cactgcagga   2340

gtctcacaag acacttcgga aaatcctaac aaaacaatag ttcctgcagc attaccacag   2400

ctcacccta ccttggtgtc actgctggag gtgattgaac ccgaggtgtt gtatgcagga   2460

tatgatagct ctgttccaga ttcagcatgg agaattatga ccacactcaa catgttaggt   2520

gggcgtcaag tgattgcagc agtgaaatgg gcaaaggcga tactaggctt gagaaactta   2580
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- 69 -

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cacctcgatg accaaatgac cctgctacag tactcatgga tgtttctcat ggcatttgcc   2640

ttgggttgga gatcatacag acaatcaagc ggaaacctgc tctgctttgc tcctgatctg   2700

attattaatg agcagagaat gtctctaccc tgcatgtatg accaatgtaa acacatgctg   2760

tttgtctcct ctgaattaca aagattgcag gtatcctatg aagagtatct ctgtatgaaa   2820

accttactgc ttctctcctc agttcctaag gaaggtctga gagccaaga  gttatttgat   2880

gagattcgaa tgacttatat caaagagcta ggaaaagcca tcgtcaaaag ggaagggaac   2940

tccagtcaga actggcaacg gttttaccaa ctgacaaagc ttctggactc catgcatgag   3000

gtggttgaga atctccttac ctactgcttc cagacatttt tggataagac catgagtatt   3060

gaattcccag agatgttagc tgaaatcatc actaatcaga taccaaaata ttcaaatgga   3120

aatatcaaaa agcttctgtt tcatcaaaaa tga                                 3153


<210>   67
<211>   1052
<212>   PRT
<213>   Saccharinycees cerevisia

<400>   67

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1               5                   10                  15


Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
            20                  25                  30


Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
            35                  40                  45


Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
    50                  55                  60


Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln
65                  70                  75                  80


Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro Gln Gly
                85                  90                  95


Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly
            100                 105                 110


Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu Asn Asp
        115                 120                 125


Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu
    130                 135                 140
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- 70 -

Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys
145   150   155   160

Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser
            165   170   175

Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu Glu Pro
            180   185   190

Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr Glu Glu
            195   200   205

Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu Ser Thr
    210   215   220

His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu Ile Lys
225   230   235   240

Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp Pro Arg Met
            245   250   255

Asp Ser Lys Glu Ser Leu Ala Pro Pro Gly Arg Asp Glu Val Pro Gly
            260   265   270

Ser Leu Leu Gly Gln Gly Arg Gly Ser Val Met Asp Phe Tyr Lys Ser
    275   280   285

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Val
    290   295   300

Ala Ala Ala Ser Gln Ala Asp Ser Lys Gln Gln Arg Ile Leu Leu Asp
305   310   315   320

Phe Ser Lys Gly Ser Thr Ser Asn Val Gln Gln Arg Gln Gln Gln Gln
            325   330   335

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro
            340   345   350

Gly Leu Ser Lys Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu
    355   360   365

Thr Glu Thr Lys Val Met Gly Asn Asp Leu Gly Tyr Pro Gln Gln Gly
    370   375   380

Gln Leu Gly Leu Ser Ser Gly Glu Thr Asp Phe Arg Leu Leu Glu Glu
385   390   395   400

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Ser Ile Ala Asn Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys
            405                 410                 415

Ser Ser Thr Ser Ala Thr Gly Cys Ala Thr Pro Thr Glu Lys Glu Phe
            420                 425                 430

Pro Lys Thr His Ser Asp Ala Ser Ser Glu Gln Gln Asn Arg Lys Ser
            435                 440                 445

Gln Thr Gly Thr Asn Gly Gly Ser Val Lys Leu Tyr Pro Thr Asp Gln
    450                 455                 460

Ser Thr Phe Asp Leu Leu Lys Asp Leu Glu Phe Ser Ala Gly Ser Pro
465                 470                 475                 480

Ala Ser Lys Asp Thr Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile
            485                 490                 495

Asp Glu Asn Leu Leu Ser Pro Leu Ala Gly Glu Asp Asp Pro Phe Leu
            500                 505                 510

Leu Glu Gly Asn Thr Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp
            515                 520                 525

Thr Lys Pro Lys Ile Lys Asp Thr Gly Asp Thr Ile Leu Ser Ser Pro
    530                 535                 540

Ser Ser Val Ala Leu Pro Gln Val Lys Thr Glu Lys Asp Asp Phe Ile
545                 550                 555                 560

Glu Leu Cys Thr Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Pro Val
            565                 570                 575

Tyr Cys Gln Ala Ser Phe Ser Gly Thr Asn Ile Ile Gly Asn Lys Met
            580                 585                 590

Ser Ala Ile Ser Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr
            595                 600                 605

His Tyr Asp Met Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys
    610                 615                 620

Pro Val Phe Asn Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp
625                 630                 635                 640

Asn Arg Cys Gln Gly Ser Gly Glu Asp Ser Leu Thr Ser Leu Gly Ala
            645                 650                 655
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Leu Asn Phe Pro Gly Arg Ser Val Phe Ser Asn Gly Tyr Ser Ser Pro
            660                 665                 670

Gly Met Arg Pro Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Ala Ala
            675                 680                 685

Thr Gly Pro Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser
            690                 695                 700

Gly Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe
705                 710                 715                 720

Lys Arg Ala Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn
            725                 730                 735

Asp Cys Ile Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg
            740                 745                 750

Tyr Arg Lys Cys Leu Gln Ala Gly Met Ala Asn Leu Glu Ala Arg Lys
            755                 760                 765

Thr Lys Lys Lys Ile Lys Gly Ile Gln Gln Ala Thr Ala Gly Val Ser
            770                 775                 780

Gln Asp Thr Ser Glu Asn Pro Asn Lys Thr Ile Val Pro Ala Ala Leu
785                 790                 795                 800

Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro
            805                 810                 815

Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Ala Trp
            820                 825                 830

Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala
            835                 840                 845

Ala Val Lys Trp Ala Lys Ala Ile Leu Gly Leu Arg Asn Leu His Leu
            850                 855                 860

Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala
865                 870                 875                 880

Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser Ser Gly Asn Leu Leu
            885                 890                 895

Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Ser Leu Pro
            900                 905                 910
```

Cys Met Tyr Asp Gln Cys Lys His Met Leu Phe Val Ser Ser Glu Leu
        915   920   925

Gln Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu
        930   935   940

Leu Leu Leu Ser Ser Val Pro Lys Glu Gly Leu Lys Ser Gln Glu Leu
945   950   955   960

Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile
                965   970   975

Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln
            980   985   990

Leu Thr Lys Leu Leu Asp Ser Met   His Glu Val Val Glu   Asn Leu Leu
        995   1000   1005

Thr Tyr   Cys Phe Gln Thr Phe   Leu Asp Lys Thr Met   Ser Ile Glu
    1010   1015   1020

Phe Pro   Glu Met Leu Ala Glu   Ile Ile Thr Asn Gln   Ile Pro Lys
    1025   1030   1035

Tyr Ser   Asn Gly Asn Ile Lys   Lys Leu Leu Phe His   Gln Lys
    1040   1045   1050

<210> 68
<211> 158
<212> PRT
<213> Saccharomycees cerevisia

<400> 68

Met Ser Thr Val Pro Leu Val Tyr Ser Pro Val Asp Arg Glu Pro Leu
1   5   10   15

His Asp Asn Ser Ala Asn Ile Lys Arg Pro Leu Gly Ser Phe Val Thr
            20   25   30

Ser Ser Ala Ala Cys Phe Lys Pro Leu Thr Ile Pro Gly Pro Thr Thr
        35   40   45

Pro Cys Ala Phe Val Met Ser Ala His Ser Ala Ile Leu Tyr Thr Pro
    50   55   60

Ala Glu Tyr Cys Asn Leu Thr Val Leu Pro Met Ser Ala Asn Phe Leu
65   70   75   80

- 74 -

Ser Ser Lys Ser Lys Lys Leu Tyr Leu Ala Asp Asn Ala Phe Ser Gly
            85   90   95

Leu Thr Val Pro Ser Met Glu Lys Ser Val Lys Ile Ser Thr Cys Val
            100   105   110

Phe Ser Lys Gln Ile Leu Gly Pro Asn Ala Ser Thr Asn Ser Ser Asn
            115   120   125

Ser Leu Val Val Arg Thr Ser Asn Glu Ala His Lys Phe Val Cys Phe
            130   135   140

Ser Cys Met Ile Leu Asn Ser Leu Ala Ala Thr Gly Leu Gly
145   150   155

<210>   69
<211>   267
<212>   PRT
<213>   Saccharomycees cerevisia

<400>   69

Met Ser Lys Ala Thr Tyr Lys Glu Arg Ala Ala Thr His Pro Ser Pro
1   5   10   15

Val Ala Ala Lys Leu Phe Asn Ile Met His Glu Lys Gln Thr Asn Leu
            20   25   30

Cys Ala Ser Leu Asp Val Arg Thr Thr Lys Glu Leu Leu Glu Leu Val
            35   40   45

Glu Ala Leu Gly Pro Lys Ile Cys Leu Leu Lys Thr His Val Asp Ile
    50   55   60

Leu Thr Asp Phe Ser Met Glu Gly Thr Val Lys Pro Leu Lys Ala Leu
65   70   75   80

Ser Ala Lys Tyr Asn Phe Leu Leu Phe Glu Asp Arg Lys Phe Ala Asp
            85   90   95

Ile Gly Asn Thr Val Lys Leu Gln Tyr Ser Ala Gly Val Tyr Arg Ile
            100   105   110

Ala Glu Trp Ala Asp Ile Thr Asn Ala His Gly Val Val Gly Pro Gly
            115   120   125

Ile Val Ser Gly Leu Lys Gln Ala Ala Glu Glu Val Thr Lys Glu Pro
            130   135   140

- 75 -

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Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Cys Lys Gly Ser Leu Ser
145             150             155             160

Thr Gly Glu Tyr Thr Lys Gly Thr Val Asp Ile Ala Lys Ser Asp Lys
            165             170             175

Asp Phe Val Ile Gly Phe Ile Ala Gln Arg Asp Met Gly Gly Arg Asp
            180             185                 190

Glu Gly Tyr Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp Asp
            195             200             205

Lys Gly Asp Ala Leu Gly Gln Gln Tyr Arg Thr Val Asp Asp Val Val
    210             215             220

Ser Thr Gly Ser Asp Ile Ile Ile Val Gly Arg Gly Leu Phe Ala Lys
225             230             235             240

Gly Arg Asp Ala Lys Val Glu Gly Glu Arg Tyr Arg Lys Ala Gly Trp
            245             250             255

Glu Ala Tyr Leu Arg Arg Cys Gly Gln Gln Asn
            260             265


<210>   70
<211>   286
<212>   PRT
<213>   Saccharomycees cerevisia

<400>   70

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1               5               10              15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
            20              25              30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
        35              40              45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
    50              55              60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65              70              75              80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
            85              90              95
```

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
            100   105   110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
            115   120   125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
        130   135   140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
145   150   155   160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
                165   170   175

Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
            180   185   190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
            195   200   205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
    210   215   220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
225   230   235   240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
            245   250   255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
            260   265   270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
            275   280   285